

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:33:43 ; Search time 43.83 Seconds
(without alignments)
490.104 Million cell updates/sec

Title: US-09-649-108-1
Perfect score: 1511
Sequence: 1 MRFVAFIFMTYWHLLNFT.....KCGIDPNSKOSDTHLEET 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1511	100.0	290	AAU03559	Human immunoregula
2	1511	100.0	290	AAE01164	Human gene 1 encod
3	1511	100.0	290	AAU01362	Human TANGO 509, a
4	1511	100.0	290	AAV72677	Human B7-4 membran
5	1511	100.0	290	AAV72645	Human B7-4 membran
6	1508	99.8	290	AAU01407	Human TANGO 509, v
7	1508	99.8	290	AAU01409	Human TANGO 509, v
8	1508	99.8	290	AAU01410	Human TANGO 509, v
9	1507	99.7	290	AAE01222	Human gene 1 encod
10	1507	99.7	290	AAU01408	Human TANGO 509, v
11	1230	81.4	235	AAE01219	Human gene 1 encod

12	1184	78.4	245	22	AAV72676	human B7-4 secrete
13	1184	78.4	245	22	AAV72644	human B7-4 secrete
14	1177	77.9	245	22	AAE01179	human gene 1 encod
15	1132	74.9	217	22	AAE01220	human gene 1 encod
16	1050	69.5	290	22	AAU03560	mouse immunoregula
17	1050	69.5	290	22	AAV72678	mouse B7-4 protei
18	1050	69.5	290	22	AAV72646	mouse B7-4 protei
19	918	60.8	176	22	AAE93439	human protein sequ
20	894.5	59.2	279	22	AAU01370	mouse TANGO 509 am
21	891.5	59.0	279	22	AAU01411	mouse TANGO 509, v
22	891.5	59.0	279	22	AAU01413	mouse TANGO 509, v
23	890.5	58.9	279	22	AAU01412	mouse TANGO 509, v
24	890.5	58.9	279	22	AAU01414	mouse TANGO 509, v
25	404	26.7	283	22	AAE01352	human gene 1 encod
26	401	26.5	233	22	AAE01415	human gene 1 encod
27	312	20.6	316	20	AAV11705	human PRO352 prote
28	312	20.6	316	21	AAE44261	human PRO352 (UNQ3
29	312	20.6	316	22	AAU00946	human B7-H3 polype
30	312	20.6	316	22	AAE87394	human gene 2 encod
31	311	20.6	534	22	AAU00906	human B lymphocyte
32	311	20.6	534	22	AAE88459	human B lymphocyte
33	311	20.6	534	22	AAE87250	human membrane or
34	309.5	20.5	1020	22	AAE37996	human amyloid prec
35	307	20.3	340	22	AAU00904	human B lymphocyte
36	307	20.3	340	22	AAU00905	human B lymphocyte
37	306	20.3	387	22	AAE87415	human gene 2 encod
38	281.5	18.6	534	22	AAE37249	human gene 2 encod
39	281	18.6	469	22	AAE11582	human amyloid prec
40	272.5	18.0	244	22	AAU00949	human B7-H3 polype
41	266.5	17.6	216	22	AAU00950	human B7-H3 polype
42	266.5	17.6	216	22	AAE87417	human gene 2 encod
43	210	13.9	524	19	AAE46488	mouse butyrophilin
44	210	13.9	524	20	AAE97816	mouse butyrophilin
45	188.5	12.5	282	21	AAE12557	human ovarian carc

ALIGNMENTS

RESULT 1	AAU03559	standard; Protein: 290 AA.
ID	AAU03559	
XX	AAU03559:	
AC		
XX		
DT	26-SEP-2001	(first entry)
XX		
DE	Human immunoregulatory protein B7-H1.	
XX		
KW	Human; immunoregulatory protein; B7-H1; co-stimulating cell;	
KW	B-cell antibody-producing response; IgG2a antibody response; AIC;	
KW	immunodeficiency disease; inflammatory disease; autoimmune disease;	
KW	antigen presenting cell; pathologic cell mediated disease.	
OS	Homo sapiens.	
XX		
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..22
FT	Protein	/label= Signal_peptide
FT		23..290
FT	Modified-site	/label= Mature_B7-H1
FT		35
FT	Domain	/note= "N-glycosylated"
FT		26..131
FT	Domain	/note= "IgV-like domain"
FT		132..234
FT	Domain	/note= "IgC-like domain"
FT		192
FT	Modified-site	/note= "N-glycosylated"
FT		200
FT	Modified-site	/note= "N-glycosylated"
FT		219
FT	Modified-site	/note= "N-glycosylated"
FT		

CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC B7-H6 secreted protein of the invention.

XX
 SQ Sequence 290 AA:

Query Match 100.0%; Score 1511; DB 22; Length 290;
 Best Local Similarity 100.0%; Pred. No. 7.3e-135;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRFAVFETMYTHLNAFVTVPRKLYVVEYSGNMTECKPEVPEKQDLALIVYWE 60
 DB 1 MRFVAVFETMYTHLNAFVTVPRKLYVVEYSGNMTECKPEVPEKQDLALIVYWE 60

(61 DKNITQVHGHEDEKQVHSSYRORARILKDLQSLGNALQTDVKTQDAGYRCMISY 120
 DB 61 dknitqvhgeedkqvhsyrrarilkdqslgnaalqtdvktqdagvrcmisy99 120

OY 121 ADYKRITVKNAPYKINQRIILVDPVTSEHETCOAGYKAEYITWSSDHOVLGK 180
 DB 121 adykrityknapynkinqriilvdpvtsehelcogaegykaeiytwssdhvlgsktt 180

OY 181 TTNKREKLENTSTLRINTTNEIFYCTFRRLDPENHNAELVPLPLAHPNERTH 240
 DB 181 ttnkreeklenstlrinttneifyctfrirlpdeenhaelvipelplahpnerth 240

OY 241 LVIIIGAILLCGVALTFEFLRKGMVDYKKGIDOTSKSKOSDPHLEET 290
 DB 241 lviiigailicgvaltfeflrkgrmvdvkkgyidotskskosdphleec 290

RESULT 3
 AAU01362
 ID AAU01362 standard; Protein: 290 AA.
 AC AAU01362;
 DT 18-JUL-2001 (first entry)
 XX
 DE Human TANGO 509 amino acid sequence.
 XX
 KW Human; TANGO 509; transmembrane protein; diagnostic; asthma;
 KW immunological disorder; arthritis; graft rejection; renal disorder;
 KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
 KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
 KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
 KW neurodegenerative disease; Parkinson's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /note= "Signal peptide"
 FT Protein 19..290
 FT /note= "Mature TANGO 509"
 FT Domain 19..240
 FT /note= "Cytoplasmic domain"
 FT Domain 33..113
 FT /note= "Immunoglobulin (Ig)-like domain"
 FT Modified-site 33..38
 FT /note= "N-myristylation site"
 FT Modified-site 35..38
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 80..82
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 105..112
 FT /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 110..115
 FT /note= "N-myristylation site"
 FT Modified-site 124..127
 FT /note= "cAMP- and cGMP-dependent prote : kinase phosphorylation site"
 FT Modified-site 127..129
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 149..152
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 168..171
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 176..178
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 184..186
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 184..187
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 192..195
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 196..198
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 200..203
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 202..205
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 210..212
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 219..222
 FT /note= "Asn is N-glycosylated"
 FT Domain 241..259
 FT /note= "Transmembrane domain"
 FT Modified-site 252..257
 FT /note= "N-myristylation site"
 FT Domain 260..290
 FT /note= "Extracellular domain"
 FT Modified-site 273..278
 FT /note= "N-myristylation site"
 FT Modified-site 279..281
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 285..288
 FT /note= "Casein kinase II phosphorylation site"

XX
 PN W0200121631-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 20-SEP-2000; 2000WO-US25982.
 XX
 PR 20-SEP-1999; 99US-0399723.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury C.
 XX
 DR WPI: 2001-211461/21.
 DR N-PSDB: AAS02076.
 XX
 PT New nucleic acid encoding INTERCEPT 307, TANGO 511, TANGO 561, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
 PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
 PT disease -
 XX
 PS Claim 8; Fig 22; 362pp; English.
 XX
 CC The sequence represents the amino acid sequence of human TANGO 509
 CC transmembrane protein. The nucleic acid and polypeptide sequences
 CC are useful for the diagnosis, prognosis and treatment of immunological
 CC disorders (e.g. arthritis, graft rejection and acquired immunodeficiency
 CC syndrome), inflammatory disorders (e.g. psoriasis and asthma), renal
 CC disorders, embryonic disorders, brain-related disorders (e.g. cerebral
 CC oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-
 CC related disorders, pituitary-related disorders (e.g. Cushing's disease)
 CC and neurodegenerative diseases (e.g. Parkinson's disease).

XX Human; B7-4 membrane protein; B7-4M; chromosome 9; antiviral; influenza;
 KW immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;
 KW graft-versus-host disease; GVHD; immunological disorder; Herpes disease;
 KW autoimmune disease; common cold; shingles disease; encephalitis; therapy;
 KW organ transplant; gene mapping; transgenic; viral infection.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Signal_peptide
 FT Protein 19..290
 FT /label= Mature_B7-4M_protein
 FT Domain 19..134
 FT /label= IGV_domain
 FT Domain 19..238
 FT /label= Extracellular_domain
 FT 135..227
 FT /label= IGC_domain
 FT 239..259
 FT /label= Transmembrane_domain
 FT 260..290
 FT /label= Cytoplasmic_domain

MO200114556-A1.

01-MAR-2001.

23-AUG-2000; 2000MO-US23256.

23-AUG-1999; 99US-0150390.

(DAND) DANA FARBER CANCER INST INC.

Freeman G, Bouslotis V, Chernova T, Malenkovich N;

WPI: 2001-202936/20.

N-PSDB; AAD02708.

PT New human B7-4 polypeptides useful for enhancing the immune response
 PT against a viral infection or induce a tumor immunity and to diagnose
 PT conditions related to aberrant B7-4 expression or activity

PS Claim 13; Fig 4; 123pp; English.

CC The present sequence is human B7-4 membrane (B7-4M) protein having a
 CC transmembrane and short cytoplasmic domain. Human B7-4 protein is
 CC isolated from human activated keratinocyte and placental cDNA libraries.
 CC B7-4 gene is localised on human chromosome 9.

CC The invention relates to human B7-4 secreted (B7-4S) protein, B7-4
 CC membrane (B7-4M) protein and their corresponding cDNA molecules. Human
 CC B7-4 proteins are useful for upregulating immune response to treat viral
 CC skin diseases such as Herpes disease or shingles disease, systemic viral
 CC diseases such as influenza, common cold and encephalitis, and for
 CC inducing tumor immunity or to downregulate an immune response useful in
 CC organ transplants, graft-versus-host disease (GVHD), treating allergies
 CC and viral infections e.g., acquired immune deficiency syndrome (AIDS).
 CC B7-4 antagonists are used to modulate the T cell co-stimulation by
 CC contacting an activated T cell with a B7-4 antigen. The invention is also
 CC used for producing non-human transgenic animals. It also provides B7-4
 CC fusion proteins which are useful for treating immunological disorders,
 CC such as autoimmune diseases or in the case of transplantation. B7-4
 CC fusion proteins are used as immunogens to produce anti-B7-4 antibodies.
 CC B7-4 cDNA is also useful for gene mapping. Methods are provided
 CC for modulating the immune response of individuals, by inhibiting or
 CC enhancing the lymphokine synthesis by the activated T cells. Diagnostic,
 CC prognostic, pharmacogenetics, screening and therapeutic methods are also
 CC provided using B7-4 proteins.

Sequence 290 AA;

Query Match 100.0%; Score 1511; DB 22; Length 290;
 Best Local Similarity 100.0%; Pred. No. 7.3e-135;
 Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIFAFTFMVTHLNLNFTVTPKDLVVEYGSNMTECKEPVEKQLD...IYWEWE 60
 DB 1 mrlfavflmtywhlnlneftvtpkdlvveysnmteckepveqldlaalivywene 60
 QY 61 DKNITGFVHGEEDLVQVSHSYQRARBLKDQLSGNALQITDVKLQDAGVRCMISYGC 120
 DB 61 dknitgfvhgeedlvqvsyqrarllkdqlsgnaqltdvklqagvrycmisysgc 120
 QY 121 ADYKRRTVKNAPYKINORILVDPVTSSEHLETCOAGEYKPAEYIWTSSDHVSGKTT 180
 DB 121 adykrirtvknaypynkinqrlivdpvtsseheltcgaeykpaeyiwtssdqhvysgktt 180
 QY 181 TTNSKREELFNVTSTLRINTTNEIFVCTFRRLDPEENHTAEVYIPPLAHPPNERHT 240
 DB 181 ttnskreelfnvtstlrlnttneifvctfrlldpeenhtaejvlpeplahppnerht 240
 QY 241 LVILGAILLCIGVALTFIRLKRGRMDYKKCGIQDTNSKKOSDTHLEET 290
 DB 241 lvilgailcligvaltfirllkrgrmmdykkcgldtnskksdthleet 290

RESULT 6

ID AAU01407 standard; Protein; 290 AA.

AC AAU01407;

DT 18-JUL-2001 (first entry)

XX Human TANGO 509, variant #1 amino acid sequence.

XX Human; TANGO 509; transmembrane protein; diagnostic; asthma;
 KW immunological disorder; arthritis; graft rejection; renal disorder;
 KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
 KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
 KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
 KW neurodegenerative disease; Parkinson's disease.

OS Homo sapiens.

PN WO200121631-A2.

PD 29-MAR-2001.

PF 20-SEP-2000; 2000MO-US25982.

PR 20-SEP-1999; 99US-0399723.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;

WPI: 2001-211461/21.

N-PSDB; AAS02118.

PT New nucleic acid encoding INTERCEPT 307, TANGO 511, TANGO 351, TANGO
 PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
 PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
 PT disease

PS Disclosure: Page 344-345; 362pp; English.

CC The sequence represents the amino acid sequence of human TANGO 509,
 CC variant #1 transmembrane protein. The nucleic acid and
 CC polypeptide sequences are useful for the diagnosis, prognosis and
 CC treatment of immunological disorders (e.g. arthritis, graft rejection and
 CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
 CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
 CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.

CC Ischaemia), tumours, prostate-related disorders, pituitary-related
CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
CC Parkinson's disease).

SO Sequence 290 AA:

Query Match 99.8%; Score 1508; DB 22; Length 290;
Best Local Similarity 99.7%; Pred. No. 1.4e-134;
Matches 289; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFAVFIFMTYWHLLNAFTVTPKDLVVEYGSNMTIECKFPVEKQJDLAALIVWEME 60
DB 1 mrlfavfifmtywhllnaftvtpkdlvveysnmtieckfpvekqjdlaalivweme 60
QY 61 DKNITQFVHGEEEDLKVOHSSYRQARLLKQDLSGNALQITDVKLQDAGYRCMISYGC 120
DB 61 dknitqfvhgeedlkvohssyrqarllkqqlsgnaalqtdvklqdagyrcmisygc 120
QY 121 ADYKRITVKNAPYKINQRIILVDPVTSSEHETLCOAGYPKAEVITSSDHQVLSGKTT 180
DB 121 adykritlevknaypnkinqrlilvdpvtseheltecgagypkaevitssdhqylsgktt 180
QY 181 TTNSKREELFNVTSTLRINTTNEIFCTFRRLDPEENHTAEVLVPELPLAMPNERTH 240
DB 181 ttnskreelfnvstlrlnttneifctfrldpeenhtaelvlpelplampnerth 240
QY 241 LVILGATLLGLVATLFIPLRKGRMDVKKCGIODNSKQSDPHLEET 290
DB 241 lvilgatlilcgvatlflirpkrgrmdvkkcgiodnsskqsdphleeth 290

RESULT 7

AAU01409 ID AAU01409 standard; protein; 290 AA.

AC AAU01409;

DT 18-JUL-2001 (first entry)

XX Human TANGO 509, variant #3 amino acid sequence.

XX Human; TANGO 509; transmembrane protein; diagnostic; asthma;
XX Immunological disorder; arthritis; graft rejection; renal disorder;
XX acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
XX AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
XX prostate; cerebrovascular disease; pituitary; Cushing's disease;
XX neurodegenerative disease; Parkinson's disease.

XX Homo sapiens.

PN WO200121631-A2.

PD 29-MAR-2001.

PF 20-SEP-2000; 2000WO-US25982.

PR 20-SEP-1999; 99US-0399723.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;

DR WPI; 2001-211461/21.

DR N-PSDB; AAS02120.

PT New nucleic acid encoding INTERCEPT 307, TANGO 511, TANGO 351, TANGO
PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease -

XX Disclosure: Page 351; 362pp; English.

CC The sequence represents the amino acid sequence of human TANGO 509,
CC variant #3 transmembrane protein. The nucleic acid and
CC polypeptide sequences are useful for the diagnosis, prognosis and
CC treatment of immunological disorders (e.g. arthritis, graft rejection and
CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
CC ischaemia), tumours, prostate-related disorders, pituitary-related
CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
CC Parkinson's disease).

SO Sequence 290 AA:

Query Match 99.8%; Score 1508; DB 22; Length 290;
Best Local Similarity 99.7%; Pred. No. 1.4e-134;
Matches 289; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRFAVFIFMTYWHLLNAFTVTPKDLVVEYGSNMTIECKFPVEKQJDLAALIVWEME 60
DB 1 mrlfavfifmtywhllnaftvtpkdlvveysnmtieckfpvekqjdlaalivweme 60
QY 61 DKNITQFVHGEEEDLKVOHSSYRQARLLKQDLSGNALQITDVKLQDAGYRCMISYGC 120
DB 61 dknitqfvhgeedlkvohssyrqarllkqqlsgnaalqtdvklqdagyrcmisygc 120
QY 121 ADYKRITVKNAPYKINQRIILVDPVTSSEHETLCOAGYPKAEVITSSDHQVLSGKTT 180
DB 121 adykritlevknaypnkinqrlilvdpvtseheltecgagypkaevitssdhqylsgktt 180
QY 181 TTNSKREELFNVTSTLRINTTNEIFCTFRRLDPEENHTAEVLVPELPLAMPNERTH 240
DB 181 ttnskreelfnvstlrlnttneifctfrldpeenhtaelvlpelplampnerth 240
QY 241 LVILGATLLGLVATLFIPLRKGRMDVKKCGIODNSKQSDPHLEET 290
DB 241 lvilgatlilcgvatlflirpkrgrmdvkkcgiodnsskqsdphleeth 290

RESULT 8

AAU01410 ID AAU01410 standard; protein; 290 AA.

AC AAU01410;

DT 18-JUL-2001 (first entry)

XX Human TANGO 509, variant #4 amino acid sequence.

XX Human; TANGO 509; transmembrane protein; diagnostic; asthma;
XX Immunological disorder; arthritis; graft rejection; renal disorder;
XX acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
XX AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
XX prostate; cerebrovascular disease; pituitary; Cushing's disease;
XX neurodegenerative disease; Parkinson's disease.

XX Homo sapiens.

PN WO200121631-A2.

PD 29-MAR-2001.

PF 20-SEP-2000; 2000WO-US25982.

PR 20-SEP-1999; 99US-0399723.

PA (MILL-) MILLENNIUM PHARM INC.

PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;

DR WPI; 2001-211461/21.

DR N-PSDB; AAS02121.

PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease -

PS Disclosure: Page 354-355; 362pp; English.

XX The sequence represents the amino acid sequence of human TANGO 509,
XX variant #4 transmembrane protein. The nucleic acid and
XX polypeptide sequences are useful for the diagnosis, prognosis and
XX treatment of immunological disorders (e.g. arthritis, graft rejection and
XX acquired immunodeficiency syndrome), inflammatory disorders (e.g.
XX psoriasis and asthma), renal disorders, embryonic disorders, brain-
XX related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
XX ischaemia), tumours, prostate-related disorders, pituitary-related
XX disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
XX Parkinson's disease).

XX Sequence 290 AA;

XX Query Match

XX Best Local Similarity 99.8%; Score 1508; DB 22; Length 290;

XX Matches 289; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1 MRIFVFRTMTWHLNATVTVPKDLVYVEGSMNTTECKRPVEKQDLALVYWE 60

XX 1 mlrlvflmlywhlnatlvtpkdlvveygsmntleckrpvqkqlaaliyywme 60

XX 61 DKNIIQFVGEEDLVQVHSSYRQARLLKDKQLSLGNAALQITDVKLQDAGVRCMISYGG 120

XX 61 dknllqfvggeedlvqvhssyrgarllkdqslsgnaalqitdvklqdgvyrcmisygg 120

XX 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETCOAESYPAEVIWTSDDVJUSGKTT 180

XX 121 adykriltvknvapykinqrllvdpvtsehelctcaeqypkaevlwtsddvjlvsqktt 180

XX 181 TTNSKREKLFVNTSLRINTTNEIFYCTFRRLDPEENHTAEVLPPLAHPPNERH 240

XX 181 ttnskreklfvntslrintttneifyctfrlldpeenhtaelvlpplahppnerh 240

XX 241 LVILGAILLCGLVALTFIFRLRKGMMDVKKCGIODTNSKOSDTHLEET 290

XX 241 lvilgailclcgvaltfifrlrkgmmdvkkcgiodtnskosdthleest 290

XX RESULT 9

XX AAE01222 standard; Protein: 290 AA.

XX AAE01222;

XX 17-JUL-2001 (first entry)

XX Human gene 1 encoded secreted protein allelic variant, SEQ ID NO:123.

XX Human: secreted protein; proliferative disorder; cancer; tumour;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angiotensin disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder;
XX endocrine disorder; infection; wound healing; vulnerability; gene therapy;
XX cell culture; chemotaxis; food additive; chromosome 9;
XX binding partner identification.

XX Homo sapiens.

XX WO200134768-A2.

XX 17-MAY-2001.

XX 01-NOV-2000; 2000WO-US30039.

XX 09-NOV-1999; 99US-0164344.

XX 07-APR-2000; 2000US-0195296.

XX 27-JUL-2000; 2000US-0221367.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Olsen HS, Komatsoulis G, Duan DR, Ebner R, Kuben St,

XX WPI, 2001-308780/32.

XX Isolated nucleic acid molecule encoding a human secreted protein is

XX used in preventing, treating or ameliorating a medical condition -

XX Disclosure: Page 8; 474pp; English.

XX AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted
XX protein genes, and AAE01164-AAE01217 represent the proteins they encode.
XX AAE01218-AAE01226 represent human secreted protein fragments or variants.
XX The secreted proteins and their genes are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 15 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angiotensin disorders, kidney disorders,
XX gastrointestinal disorders, pregnancy-related disorders, endocrine
XX disorders, and infections. The proteins can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin aging due to
XX sunburn, to maintain organs before transplantation, to improve cell
XX culture of primary tissues, to regenerate tissues, to identify their
XX cognate ligands or binding partners, and in chemotaxis, and can be used
XX as a food additive or preservative to modify storage properties.

XX Antibodies specific for a protein of the invention can be used in
XX alleviating symptoms associated with the disorders mentioned above, and
XX in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX immunosorbent assay (ELISA). The present sequence represents a human
XX secreted protein allelic variant of B7-H6 protein referred to in the
XX disclosure of the invention.

XX Sequence 290 AA;

XX Query Match 99.7%; Score 1507; DB 22; Length 290;

XX Best Local Similarity 99.7%; Pred. No. 1.7e-134;

XX Matches 289; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 MRIFVFRTMTWHLNATVTVPKDLVYVEGSMNTTECKRPVEKQDLALVYWE 60

XX 1 mlrlvflmlywhlnatlvtpkdlvveygsmntleckrpvqkqlaaliyywme 60

XX 61 DKNIIQFVGEEDLVQVHSSYRQARLLKDKQLSLGNAALQITDVKLQDAGVRCMISYGG 120

XX 61 dknllqfvggeedlvqvhssyrgarllkdqslsgnaalqitdvklqdgvyrcmisygg 120

XX 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETCOAESYPAEVIWTSDDVJUSGKTT 180

XX 121 adykriltvknvapykinqrllvdpvtsehelctcaeqypkaevlwtsddvjlvsqktt 180

XX 181 TTNSKREKLFVNTSLRINTTNEIFYCTFRRLDPEENHTAEVLPPLAHPPNERH 240

XX 181 ttnskreklfvntslrintttneifyctfrlldpeenhtaelvlpplahppnerh 240

XX 241 LVILGAILLCGLVALTFIFRLRKGMMDVKKCGIODTNSKOSDTHLEET 290

[illegible]

Db	121	adjrltvcvknaypknqngcllvdpvtsheheltcgaeygpkcevwltwssbqvlvsqklt	180
Qy	181	TTNSKREEEKLFENVTSTLRITNTTNEIFCYCFRRLRDPEENITAEVLVPELPLAPIPRNERH	240
Db	181	ltmskreelklnvstslrlntltneftfcfftrldpeentveelviipeipiahppnerth	240
Qy	241	LVIGAILLCIGVALTFPIFLRKGRMMDVKKCIQPTNSKSKQSDTHLEET	290
Db	241	lvilgailllcigvaltfflfrgrmmdvkkqigdtnskksqsdthleel	290
RESULT	11		
ID	AAE01219	standard; Protein: 235 AA.	
XX	AAE01219;		
XX	17-JUL-2001	(first entry)	
DE	Human gene 1	encoded secreted protein fragment, SEQ ID NO:120.	
KW	Human: secreted protein; proliferative disorder; cancer; tumour;		
KW	fetal abnormality; developmental abnormality; haematopoietic disorder;		
KW	immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;		
KW	Inflammation; allergy; neurological disorder; Alzheimer's disease;		
KW	Parkinson's disease; cognitive disorder; schizophrenia; asthma;		
KW	skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;		
KW	cardiovascular disorder; angiogenic disorder; kidney disorder;		
KW	gastrointestinal disorder; pregnancy-related disorder;		
KW	endocrine disorder; infection; wound healing; viderinary; gene therapy;		
KW	cell culture; chemotaxis; food additive; chromosome 9;		
XX	binding partner identification.		
XX	Homo sapiens.		
XX	MO200134768-A2.		
XX	17-MAY-2001.		
XX	01-NOV-2000; 2000MO-U0530039.		
XX	09-NOV-1999; 9905-0164344.		
XX	07-APR-2000; 20000US-0195296.		
XX	27-JUL-2000; 20000US-0221367.		
XX	(HUMA-) HUMAN GENOME SCT INC.		
XX	Olssen HS, Komatsoulis G, Duan DR, Ebner R, Ruben SM;		
XX	WPI; 2001-308780/32.		
XX	Isolated nucleic acid molecule encoding a human secreted protein is		
XX	used in preventing, treating or ameliorating a medical condition		
XX	Disclosure: Page 8; 474pp; English.		
XX	AA005053-AA005106 represent cDNAs corresponding to 15 human secreted		
XX	protein genes, and AAE01164-AAE01217 represent the proteins they encode.		
XX	AAE01218-AAE01226 represent human secreted protein fragments or variants		
XX	The secreted proteins and their genes are useful for preventing,		
XX	treating or ameliorating medical conditions, e.g., by protein or gene		
XX	therapy. Pathological conditions can be diagnosed by determining the		
XX	amount of the new protein in a sample or by determining the presence of		
XX	mutations in the new genes. Specific uses are described for each of the		
XX	15 genes, based on the tissues in which they are most highly expressed,		
XX	and include developing products for the diagnosis or treatment of		
XX	proliferative disorders, cancer, tumours, fetal and developmental		
XX	abnormalities, haematopoietic disorders, diseases of the immune system,		
XX	AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,		
XX	allergies, neurological disorders (e.g., Alzheimer's disease,		
XX	Parkinson's disease), cognitive disorders, schizophrenia, asthma,		
XX	skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,		
XX	cardiovascular disorders, angiogenic disorders, kidney disorders,		

CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein fragment which is the extracellular domain of B7-H6
CC protein referred to in the disclosure of the invention.

CC Sequence 235 AA:

Query Match 81.4%; Score 1230; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,1e-108;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 1 MRIFAVFIEMTYWHLNMFYTVVPRKDLVVEGSMWTECKRPVKQDLALITYWEME 60
D 1 mrlavflmtywhlnmfvtvvpkdlvvegsmwteckrpvkdlaalivyweme 60
Q 61 DKNITQFVHGEEDLKVOHSSYRQARLLKDLQSLGNALQITDVYKLODAGVYRCMISYGG 120
D 61 dknitqfvhgeedlkvghssyrqarllkdqslgnalqitdvylodagvyrcmisygg 120
Q 121 ADYKRITVKNVAPYKINORILLVDPVTSSEHETLCOAGCYPRAEVIWTSQHVLGKRTT 180
D 121 adykrityknvapykinqrillvdpvtsehelctcgaeypraeviwtsqhvlgskrtt 180
Q 181 TTNSKREELFNWSTLRINTTNEIFCTPRRLDPEENHRAELVIRPELPAHPP 235
D 181 ttnskreelfnwstlrinttneifctprrrldpeenhraelvipeelpahpp 235

RESULT 12

ID AAY72676
AA72676 standard; Protein: 245 AA.

XX AAY72676;

DT 19-JUN-2001 (first entry)

DE Human B7-4 secreted (B7-4S) protein.

XX Human; B7-4 secreted protein; B7-4S; receptor PD-1; chromosome 9; tumour;
XX antiviral; anti-allergic; gene mapping; cytostatic; myocardial infarction;
XX atherosclerosis; neurological disease; immunomodulatory; allergy; GVHD;
XX graft-versus-host disease; immunosuppressive disease; organ transplant;
XX acquired immune deficiency syndrome; AIDS; autoimmune disease; therapy.

XX Homo sapiens.

XX OS Location/Qualifiers

XX Key 1.18

XX Peptide /label= Signal_peptide

XX Protein 19..245

XX /label= Mature_B7-4S_protein

XX /note= "Serves as an extracellular domain"

XX Domain 19..134

XX /label= Igy_domain

XX Domain 135..227

XX /label= Igc_domain

XX Region 228..245

XX /note= "Hydrophilic tail"

XX WO200114557-A1.

XX 01-MAR-2001.

PF 23-AUG-2000; 2000WO-US23347.
XX 23-AUG-1999; 99US-0150390.
PR 10-NOV-1999; 99US-0164897.

XX (DAND) DANA FARBER CANCER INST INC.
XX (GEWY) GENETICS INST INC.

PI Wood C, Freeman GJ;

XX WPI: 2001-160116/16.

DR N-PSDB; AAD02772.

PT Treating e.g. cancer or allergies comprises contacting an immune cell
PT with an agent that modulates signaling via PD-1 or B7-4 to modulate the
PT immune response -

XX Example 1; Fig 3; 168pp; English.

CC The present sequence is human B7-4 secreted (B7-4S) protein having a
CC short hydrophilic tail without a membrane anchor or a transmembrane
CC domain. The human B7-4 cDNA is isolated from human activated Keratinocyte
CC and placental cDNA libraries. B7-4 gene is localised on human
CC chromosome 9.

CC The invention relates to a method for modulating immune response by
CC contacting an immune cell with an agent that modulates signaling via
CC B7-4 or its receptor PD-1. Modulating the interaction between PD-1 and
CC B7-4 modulates a costimulatory or an inhibitory signal in an immune cell,
CC resulting in the modulation of the immune response. The invention is
CC useful for upregulating an immune response to treat tumours, neurological
CC diseases and immunosuppressive diseases or to downregulate an immune
CC response useful in organ transplants, graft-versus-host disease (GVHD),
CC treating allergies and viral infections e.g., acquired immune deficiency
CC syndrome (AIDS). The invention also provides B7-4 or PD-1 fusion proteins
CC which are useful for treating immunological disorders, such as autoimmune
CC diseases e.g., heart disease, myocardial infarction and atherosclerosis
CC or in the case of inhibiting rejection of transplants. These fusion
CC proteins are also used as immunogens to produce anti-B7-4 antibodies.
CC PD-1 is useful in promoting the maintenance of pregnancy. B7-4 protein is
CC highly expressed in placental trophoblasts and plays a role in preventing
CC maternal rejection of the foetus. B7-4 cDNA is also useful for
CC gene mapping.

XX Sequence 245 AA:

Query Match 78.4%; Score 1184; DB 22; Length 245;
Best Local Similarity 100.0%; Pred. No. 5,1e-104;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 1 MRIFAVFIEMTYWHLNMFYTVVPRKDLVVEGSMWTECKRPVKQDLALITYWEME 60
D 1 mrlavflmtywhlnmfvtvvpkdlvvegsmwteckrpvkdlaalivyweme 60
Q 61 DKNITQFVHGEEDLKVOHSSYRQARLLKDLQSLGNALQITDVYKLODAGVYRCMISYGG 120
D 61 dknitqfvhgeedlkvghssyrqarllkdqslgnalqitdvylodagvyrcmisygg 120
Q 121 ADYKRITVKNVAPYKINORILLVDPVTSSEHETLCOAGCYPRAEVIWTSQHVLGKRTT 180
D 121 adykrityknvapykinqrillvdpvtsehelctcgaeypraeviwtsqhvlgskrtt 180
Q 181 TTNSKREELFNWSTLRINTTNEIFCTPRRLDPEENHRAELVIRPELPAHPP 227
D 181 ttnskreelfnwstlrinttneifctprrrldpeenhraelvipeelpahpp 227

RESULT 13

ID AAY72644
AA72644 standard; Protein: 245 AA.

XX AAY72644;

XX

DT	31-MAY-2001	(first entry)
XX		
DE	Human B7-4 secreted (B7-4S) protein.	
XX		
KW	Human; B7-4 secreted protein; B7-4S; chromosome 9; antiviral; influenza;	
KW	immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;	
KW	grafft-versus-host disease; GVHD; immunological disorder; Herpes disease;	
KW	autoimmune disease; common cold; shingles disease; encephalitis; therapy;	
KW	organ transplant; gene mapping; transgenic; viral infection.	
XX		
OS	Homo sapiens.	
XX		
FI	Key	Location/Qualifiers
FT	Peptide	1..18
FT	Protein	/label= Signal_peptide
FT		19..245
FT		/label= Mature_B7-4S-protein
FT		/note= "Serves as an extracellular domain"
FT	Domain	19..134
FT	Domain	/label= IgV_domain
FT		135..227
FT	Region	/label= IgC_domain
FT		228..245
FT		/note= "Hydrophilic tail"
XX		
PN	WO200114556-A1.	
PD	01-MAR-2001.	
XX		
PF	23-AUG-2000; 2000WO-US23256.	
XX		
PR	23-AUG-1999; 99US-0150390.	
XX		
PA	(DAND) DANA FARBER CANCER INST INC.	
PI	Freeman G, Boussiotis V, Chernova T, Malenkovich N;	
DR	WPI: 2001-202936/20.	
XX	N-PSDB: AAD02707.	
PT	New human B7-4 polypeptides useful for enhancing the immune response	
PT	against a viral infection or induce a tumor immunity and to diagnose	
PT	conditions related to aberrant B7-4 expression or activity	
XX		
PS	Claim 13; Fig 3; 123pp; English.	
XX		
CC	The present sequence is human B7-4 secreted (B7-4S) protein having a	
CC	short hydrophilic tail without a membrane anchor or a transmembrane	
CC	domain. Human B7-4 protein is isolated from human activated keratinocyte	
CC	and placental cDNA libraries. B7-4 gene is localised on human	
CC	chromosome 9.	
CC	The invention relates to human B7-4 secreted (B7-4S) protein, B7-4	
CC	membrane (B7-4M) protein and their corresponding cDNA molecules. Human	
CC	B7-4 proteins are useful for upregulating immune response to treat viral	
CC	skin diseases such as Herpes disease or shingles disease, systemic viral	
CC	diseases such as influenza, common cold and encephalitis, and for	
CC	inducing tumour immunity or to downregulate an immune response useful in	
CC	organ transplants, graft-versus-host disease (GVHD), treating allergies	
CC	and viral infections e.g., acquired immune deficiency syndrome (AIDS).	
CC	B7-4 antagonists are used to modulate the T cell co-stimulation by	
CC	contacting an activated T cell with a B7-4 antigen. The invention is also	
CC	used for producing non-human transgenic animals. It also provides B7-4	
CC	fusion proteins which are useful for treating immunological disorders,	
CC	such as autoimmune diseases or in the case of transplantation. B7-4	
CC	fusion proteins are used as immunogens to produce anti-B7-4 antibodies.	
CC	B7-4 cDNA is also useful for gene mapping. Methods are provided	
CC	for modulating the immune response of individuals, by inhibiting or	
CC	enhancing the lymphocyte synthesis by the activated T cells. Diagnostic,	
CC	prognostic, pharmacogenetics, screening and therapeutic methods are also	
CC	provided using B7-4 proteins.	
XX		
SO	Sequence 245 AA:	

Query Match	Similarity	78.4%	Score 1184	DB 22	Length 245
Best Local	Similarity 100.0%	Pred. No. 5	1e-104		
Matches	227	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	MRFAVEFTMTYWHLLNAFTVTPKDLVYVEYGSNMVTECKFPEVKQDLDAALIVYWEHE	60		
DB	1	mlfavlftfemywhllnaftfvcpxdlyyveygsnmfleckfpevkqdlldaalivywehe	60		
QY	61	DKNIITQFNGCEDLTVONHSSYRQRYRLILKDLQSLGNAALQITPDVKIOLVAGVYRCMTSYGC	120		
DB	61	dknllqfivngcedltvqnhssyqrarllkdqlslgnaalqltdcvkfgdqdyvrcmtsygg	120		
QY	121	ADYKRITKYVNAFYNNKIQRLILVDPVTSSEHLETCQAEGYPRAEVYIWTSSDHOVLGKTT	180		
DB	121	adykrilkyvnaarykngirlvdpvtsehealtcqaegypraevalwtssdqvlsgktt	180		
QY	181	TNNSKREEKLENVSTSLRINTNTTNEFLVCTVSPRRDLRENNHTAEVYIP	227		
DB	181	tnnskreeklenvstslrlnnttneelfvctfrrldpreennhtaelvyp	227		

PT used in preventing, treating or ameliorating a medical condition
XX
XX Claim 11; Page 454; 474pp; English.

CC AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted
CC protein genes, and AAE01164-AAE01217 represent the proteins they encode.
CC AAE01218-AAE01226 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 15 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumors, foetal and developmental
CC abnormalities, hematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays (e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA)). The present sequence represents a human
CC B7-H6 secreted protein of the invention.

XX Sequence 245 AA:

Query Match 77.9%; Score 1177; DB 22; Length 245;
Best Local Similarity 99.6%; Pred. No. 2,3e-103;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFAVFPTMYWHLINAFVTPVKDLYVEYGSNMTFECKPEVKOLDLALIVYEMEK 60
DB 1 mlifavflmtywhlinaltvtvpxdlyvveysnmtleckfpvekqlaalliyweme 60
QY 61 DNIIIOFVGEEDLKVOHSEYRORARLLKDOIISGNAALITDVKODAGVRCMISYSG 120
DB 61 dniiiofivgeedlkvoqhsyrrgrallkqqlisgnaalqldvkiqdaaxyrcmisyg 120
QY 121 ADYKRITVKNAPYKNINORILVVPVTSSEHETLCOAEGYPRAEVITWSSDHQVLSGKT 180
DB 121 adykrityvknapykninorilvvpvtsseheltcoagypkaevitwssdhqivlsqklt 180
QY 181 TTNSSREKLFNVSTSLKINTTTNEIFCTFRRLDPENHFAELVIP 227
DB 181 ttnssreklfnvstslkintttneifctfrldpeenhfaelvip 227

RESULT 15
AAE01220 standard: Protein; 217 AA.

XX AAE01220;

XX 17-JUL-2001 (first entry)

DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:121.

KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;

KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery; gene therapy;
KW cell culture; chemotaxis; food additive; chromosome 9;
KW binding partner identification.

XX Homo sapiens.
XX WO200134766-A2.

XX 17-MAY-2001.

XX 01-NOV-2000; 2000WO-US30039.

XX 09-NOV-1999; 99US-0164344.

XX 07-APR-2000; 2000US-0195296.

XX 27-JUL-2000; 2000US-0221367.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Olsen HS, Komatsoulis G, Duan DR, Ebner R, Ruben SM;
XX WPI; 2001-308780/32.

XX Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition

XX Disclosure; Page 8-9; 474pp; English.

CC AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted
CC protein genes, and AAE01164-AAE01217 represent the proteins they encode.
CC AAE01218-AAE01226 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 15 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumors, foetal and developmental
CC abnormalities, hematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays (e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA)). The present sequence represents a human
CC secreted protein fragment which is the mature extracellular domain of
CC B7-H6 protein referred to in the disclosure of the invention.

XX Sequence 217 AA:

Query Match 74.9%; Score 1132; DB 22; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-99;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 FMYTVKRDLYVVEYGSNMTFECKPEVKOLDLALIVYEMEKNIIOFVHGEEDLKVOH 78

DB 1 fmytvkrdlyvveysnmtleckfpvekqlaalliywemedkniiofivhgeedlkvoq 60

QY 79 SSYRORARLLKDOIISGNAALITDVKODAGVRCMISYGDADYKRIYVKNAPYKNIN 138

Db 61 syyqra1lkdg1sgnaalqldcvk1qdagvyrcmisy9gadykrltvkvnapykn1n 120
QY 139 ORLWDPVPTSEHETCOAEQYPKAEVIMTSSDHQVLSGKTTTNSKREKLFNVTSTLR 198
Db 121 qrlivdpvsehelccgaegypkaevlwcssdhqvlsgkcttcnskreek1fnvsc1r 180
QY 199 INTTNEIFYCTFRRRLDPEENHTAELV1PELPLAHP 235
Db 181 Inttneifyctfrrldpeenhtaevl1pelplahpp 217

Search completed: March 18, 2002, 06:34:57
Job time: 74 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:33:43 ; Search time 26.9 Seconds
(without alignments)
242.601 Million cell updates/sec

Title: US-09-649-108-1

Perfect score: 1511

Sequence: 1 MRFAVFIIMTYWHLLNAFT.....KCIQDPTNSKKSDTHLEET 290

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

1 number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_patents_AA.*
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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177.5	11.7	306	2	US-08-147-772-4 Sequence 4, Appli
2	177.5	11.7	306	2	US-08-456-104-8 Sequence 8, Appli
3	177.5	11.7	306	2	US-08-101-624-25 Sequence 25, Appli
4	177.5	11.7	306	3	US-08-153-262-4 Sequence 4, Appli
5	177.5	11.7	306	3	US-08-479-744A-31 Sequence 31, Appli
6	177.5	11.7	306	4	US-08-280-757B-31 Sequence 31, Appli
7	177.5	11.7	306	4	US-09-159-115-4 Sequence 4, Appli
8	177.5	11.7	306	2	US-08-147-772-2 Sequence 2, Appli
9	177.5	11.7	306	2	US-08-456-104-6 Sequence 6, Appli
10	177.5	11.7	306	2	US-08-101-624-23 Sequence 23, Appli
11	177.5	11.7	306	3	US-08-153-262-2 Sequence 6, Appli
12	177.5	11.7	306	3	US-08-479-744A-29 Sequence 29, Appli
13	177.5	11.7	306	4	US-08-280-757B-29 Sequence 29, Appli
14	177.5	11.7	306	4	US-09-159-115-2 Sequence 2, Appli
15	177.5	11.7	306	4	US-08-205-697A-19 Sequence 19, Appli
16	177.5	11.7	306	4	US-08-702-525-19 Sequence 19, Appli
17	177.5	11.7	306	4	US-08-702-525-17 Sequence 17, Appli
18	177.5	11.7	306	4	US-08-702-525-17 Sequence 17, Appli
19	169.5	11.2	306	4	US-08-702-525-17 Sequence 17, Appli
20	169.5	11.2	306	5	PCT-US95-02576-17 Sequence 17, Appli
21	169.5	11.2	306	5	PCT-US95-02576-17 Sequence 17, Appli
22	169.5	11.2	306	5	PCT-US95-02576-17 Sequence 17, Appli
23	169.5	11.2	306	5	PCT-US95-02576-2 Sequence 2, Appli
24	169.5	11.2	306	5	PCT-US95-02576-2 Sequence 2, Appli
25	161.5	10.7	323	5	PCT-US94-09642-2 Sequence 2, Appli
26	161.5	10.7	329	2	US-08-456-104-2 Sequence 2, Appli
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28	161.5	10.7	329	3	US-08-479-744A-2 Sequence 2, Appli
29	161.5	10.7	329	4	US-08-280-757B-2 Sequence 2, Appli
30	161.5	10.7	329	4	US-08-205-697A-23 Sequence 23, Appli
31	161.5	10.7	329	4	US-08-702-525-23 Sequence 23, Appli
32	161.5	10.7	329	5	PCT-US95-02576-23 Sequence 23, Appli
33	158.5	10.5	208	3	US-08-630-172-15 Sequence 15, Appli
34	158.5	10.5	208	4	US-09-375-419-15 Sequence 15, Appli
35	156.5	10.4	473	4	US-09-171-945-131 Sequence 131, App
36	154.5	10.2	589	2	US-08-724-394A-1 Sequence 1, Appli
37	144	9.5	581	2	US-08-724-394A-3 Sequence 3, Appli
38	140	9.3	365	4	US-08-928-383B-2 Sequence 2, Appli
39	139.5	9.2	319	1	US-08-597-495B-22 Sequence 22, Appli
40	139.5	9.2	319	4	US-09-068-051A-22 Sequence 22, Appli
41	138	9.1	581	2	US-08-724-394A-2 Sequence 2, Appli
42	137	9.1	365	2	US-08-979-424-3 Sequence 3, Appli
43	137	9.1	365	4	US-09-272-456-2 Sequence 2, Appli
44	133.5	8.8	318	4	US-09-068-051A-32 Sequence 32, Appli
45	127.5	8.4	309	2	US-08-456-104-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-147-772-4
Sequence 4, Application US/08147772
Patent No. 5858776
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasthranmanan
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immune Reactivity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B lymphocyte activation antigen; Ig
DESCRIPTION: superfamily member; T cell costimulatory signal
DESCRIPTION: via activation of CD28 pathways, binds to, CD28+
FEATURE:
NAME/KEY: signal sequence

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LOCATION: -37 to -1
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 210
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 211 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular (cytoplasmic) domain
LOCATION: 236 to 269
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 105
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 106 to 199
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: GRAY, GARY S.
AUTHORS: GIMMI, CLAUDE D.
AUTHORS: LOMBARD, DAVID B.
AUTHORS: ZHOU, LIANG-JI
AUTHORS: WHITE, MICHAEL
AUTHORS: FINGERROTH, JOYCE D.
AUTHORS: GRIBBEN, JOHN G.
AUTHORS: NADLER, LEE M.
TITLE: Structure, Expression, and T Cell Costimulatory
TITLE: Activity Of The Murine Homologue Of The Human B7
JOURNAL: Journal of Experimental Medicine
VOLUME:
ISSUE:
PAGES:
DATE: IN PRESS
RELEVANT RESIDUES IN SEQ ID NO: 4: From -37 to 269
147-772-4

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APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
DESCRIPTION: B lymphocyte activation antigen; Ig
DESCRIPTION: superfamily member; T cell costimulatory signal
DESCRIPTION: via activation of CD28 pathways, binds to CD28+
DESCRIPTION: T cells, transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -37 to -1
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 210
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 211 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular (cytoplasmic) domain
LOCATION: 236 to 269
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 105
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 106 to 199
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:

AUTHORS: FREEMAN, GORDON J.
AUTHORS: GRAY, GARY S.
AUTHORS: GIMAI, CLAUDE D.
AUTHORS: LOMBARD, DAVID B.
AUTHORS: ZHOU, LIANG-JI
AUTHORS: WHITE, MICHAEL
AUTHORS: FINGEROTH, JOYCE D.
AUTHORS: GRIEBEN, JOHN G.
AUTHORS: NADLER, LEE M.
TITLE: Structure, Expression, and T Cell Costimulatory
TITLE: Activity Of The Murine Homologue Of The Human B
TITLE: Lymphocyte Activation Antigen B7
JOURNAL: Journal of Experimental Medicine
VOLUME:
ISSUE:
PAGES:
DATE: IN PRESS
RELEVANT RESIDUES IN SEQ ID NO: 25: From -37 to 269
US-08-101-624-25
Query Match 11.7%; Score 177.5; DB 2; Length 306;
Best Local Similarity 26.6%; Pred. No. 4.2e-10;
Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11;
QY 55 VYMEMEDKNIIOFVGEEDLKQVHSSYRQRARLLDQSLGNAALQITDYKLDGAYRC 114
DB 68 IYOKHDKVYLSVIAGK-LKV-WPEYKRT--LYDNTTY---SILILGLVLSDKGTYSQ 119
QY 115 MI-----SYGADYKRIYKVNAVYKINQRIILVVD---PYTSHSLTCQAF-CYPAE 164
DB 120 VYOKKERGTGYKHLALVKSIAKADFPN---ITSEGNFSAADIKRIITCFASGQFPNR 175
QY 165 VIWISSDHOVLSGKTTTNSKREKLFNVTSLRINTTNEIFYCI FRRLDILENHTAE 224
DB 176 FSWLENGRE-LPGINTTISODESELYTISOLDENFTFNHTIKCLIKYGD---HVSBD 231
QY 225 VPEPLAHPPNERHIVILGAILICIGALFPI 258
DB 232 FTWEKPEDDPDSKNTLVFGA---GFGAVITV 262
RESULT 4
US-08-153-262-4
Sequence 4, Application US/08153262
Patent No. 6071716
GENERAL INFORMATION:
APPLICANT: FREEMAN, GORDON J.
APPLICANT: FREEDMAN, ARNOLD S.
APPLICANT: NADLER, LEE M.
TITLE OF INVENTION: DNA Encoding B7, A New Member
TITLE OF INVENTION: OF The IgG Superfamily With Unique Expression On
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30
OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,262
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991

```

1  ATTORNEY/AGENT INFORMATION:
2  NAME: HART, JULIA D.
3  REGISTRATION NUMBER: 33132
4  REFERENCE/DOCKET NUMBER: DFCI-116.1
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: (203) 255-8900
7  TELEFAX: (203) 259-2846
8  INFORMATION FOR SEQ ID NO: 4:
9  SEQUENCE CHARACTERISTICS:
10  LENGTH: 306 amino acids
11  TYPE: amino acid
12  TOPOLOGY: linear
13  MOLECULE TYPE: protein
14  DESCRIPTION: B lymphocyte activation antigen; Ig
15  DESCRIPTION: superfamily member; T cell costimulatory signal
16  DESCRIPTION: via activation of CD28 pathways, binds to CD28+
17  DESCRIPTION: T cells, transmembrane protein
18  FEATURE:
19  NAME/KEY: signal sequence
20  LOCATION: -37 to -1
21  IDENTIFICATION METHOD: similarity with known
22  IDENTIFICATION METHOD: sequence
23  OTHER INFORMATION: hydrophobic
24  FEATURE:
25  NAME/KEY: extracellular domain
26  LOCATION: 1 to 210
27  IDENTIFICATION METHOD: similarity with known
28  IDENTIFICATION METHOD: sequence
29  FEATURE:
30  NAME/KEY: transmembrane domain
31  LOCATION: 211 to 235
32  IDENTIFICATION METHOD: similarity with known
33  IDENTIFICATION METHOD: sequence
34  FEATURE:
35  NAME/KEY: intracellular (cytoplasmic) domain
36  LOCATION: 236 to 269
37  IDENTIFICATION METHOD: similarity with known
38  IDENTIFICATION METHOD: sequence
39  FEATURE:
40  NAME/KEY: Ig V-set domain
41  LOCATION: 1 to 105
42  IDENTIFICATION METHOD: similarity with known
43  IDENTIFICATION METHOD: sequence
44  FEATURE:
45  NAME/KEY: Ig C-set domain
46  LOCATION: 106 to 199
47  IDENTIFICATION METHOD: similarity with known
48  IDENTIFICATION METHOD: sequence
49  PUBLICATION INFORMATION:
50  AUTHORS: FREEMAN, GORDON J.
51  AUTHORS: GRAY, GARY S.
52  AUTHORS: GIMMI, CLAUDE D.
53  AUTHORS: LOMBARD, DAVID B.
54  AUTHORS: ZHOU, LIANG-JI
55  AUTHORS: WHITE, MICHAEL
56  AUTHORS: FINGEROTH, JOYCE D.
57  AUTHORS: GRIBBEN, JOHN G.
58  AUTHORS: NADLER, LEE M.
59  TITLE: Structure, Expression, and T Cell Costimulatory
60  TITLE: Activity Of The Murine Homologue Of The Human B
61  TITLE: Lymphocyte Activation Antigen B7
62  JOURNAL: Journal of Experimental Medicine
63  VOLUME:
64  ISSUE:
65  PAGES:
66  DATE: IN PRESS
67  RELEVANT RESIDUES IN SEQ ID NO: 4: From -37 to 269
68  US-08-153-262-4
69  Query Match 11.7%; Score 177.5; DB 3; Length 306;
70  Best Local Similarity 26.6%; Pred. No. 4.2e-10;
71  Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11.

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01 55 YWMEHEDNIIIOFVGEEDLKVHOSHSYRQARLLDKDLSGNMALTQTDVKKLDQAGYRC 114
02 68 IYWKQHKDKVLYSLVYAGK--LKV-WPEYKRNRI--LYDMTTY---SLILGLGLVLSNRYTSC 119
03 115 MI-----SYGADYKRYTVKVNAPYKINQRIILVVD--PVTSEHETGQAR-GYPAKE 164
04 165 VIMTSSDHQVLSGKTTTNSRREKLFNVVSTLAINTTNTEIVYCTPRRLDPENNTIAEL 224
05 176 FSWLENGRE-LPGINVTTSQDESELYTSSQDLDFNTRNHTIKLKLKYGDA--HVSED 231
06 225 VPELPLAHPENRTHVILCAAILLCGVALTFI 258
07 232 FTWEKRPEDPDPSKNTLVLPFA---GRCGAVITVV 262
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09 RESULT 5
10 : Sequence 31, Application US/08479744A
11 : Patent No. 6084067
12
13 GENERAL INFORMATION:
14 : APPLICANT: Freeman, Gordon J.
15 : APPLICANT: Nadler, Lee M.
16 : APPLICANT: Gray, Gary S.
17 : TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
18 : TITLE OF INVENTION: Uses Therefor
19 : NUMBER OF SEQUENCES: 55
20
21 CORRESPONDENCE ADDRESS:
22 : ADDRESSEE: LAHIVE & COCKFIELD, LLP
23 : STREET: 60 State Street
24 : CITY: Boston
25 : STATE: Massachusetts
26 : COUNTRY: USA
27 : ZIP: 02109
28
29 COMPUTER READABLE FORM:
30 : MEDIUM TYPE: Floppy disk
31 : COMPUTER: IBM PC compatible
32 : OPERATING SYSTEM: PC-DOS/MS-DOS
33 : SOFTWARE: PatentIn Release #1.0, Version #1.25
34
35 CURRENT APPLICATION DATA:
36 : APPLICATION NUMBER: US/08/479,744A
37 : FILING DATE: June 7, 1995
38 : CLASSIFICATION: 435
39
40 PRIOR APPLICATION DATA:
41 : APPLICATION NUMBER: 08/280,757
42 : FILING DATE: 26-JUL-1994
43 : APPLICATION NUMBER: 08/109,393
44 : FILING DATE: 28-AUG-1993
45 : APPLICATION NUMBER: 08/101,624
46 : FILING DATE: 26-JULY-1993
47 : APPLICATION NUMBER: 08/147,773
48 : FILING DATE: 3-NOV-1993
49
50 ATTORNEY/AGENT INFORMATION:
51 : NAME: Mandragouras, Amy E.
52 : REGISTRATION NUMBER: 36,207
53 : REFERENCE/DOCKET NUMBER: RPI-004CP3
54 : TELECOMMUNICATION INFORMATION:
55 : TELEPHONE: (617) 227-7400
56 : TELEFAX: (617) 227-5941
57
58 INFORMATION FOR SEO ID NO: 31:
59 : SEQUENCE CHARACTERISTICS:
60 : LENGTH: 306 amino acids
61 : TYPE: amino acid
62 : TOPOLOGY: Linear
63
64 MOLECULE TYPE: protein
65 : DESCRIPTION: B lymphocyte activation antigen; Ig
66 : DESCRIPTION: superfamily member; T cell costimulator; signal
67 : DESCRIPTION: via activation of CD28 pathways, binds to CD28+
68 : DESCRIPTION: T cells, transmembrane protein
69
70 FEATURE:
71 : NAME/KEY: signal sequence
72

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NAME/KEY: Ig V-set domain
LOCATION: 1 to 105
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 106 to 199
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: GRAY, GARY S.
AUTHORS: GIMMI, CLAUDE D.
AUTHORS: LOMBARD, DAVID B.
AUTHORS: ZHOU, LIANG-JI
AUTHORS: WHITE, MICHAEL
AUTHORS: FINGEROTH, JOYCE D.
AUTHORS: GRIBBEN, JOHN G.
AUTHORS: NADLER, LEE M.
TITLE: Structure, Expression, and T Cell Costimulatory
TITLE: Activity Of The Murine Homologue Of The Human B
JOURNAL: Journal of Experimental Medicine
VOLUME:
ISSUE:
PAGES:
DATE: IN PRESS
RELEVANT RESIDUES IN SEQ ID NO: 31: From -37 to 269
US-08-280-757B-31

Query Match      11.7%; Score 177.5; DB 4; Length 306;
Best Local Similarity 26.6%; Pred. No. 4.2e-10;
Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11;

QY 55 VYMEEDKNIQFVHGDEPKVQSSYRQARLKLKDLQSGNALQITDYLQDAGVYRC 114
DB 68 IYWKHKDVVLSYAGK-LKV-WPEYKNT--LYDNTTY--SLILGLVLSRGYISC 119
QY 115 MI-----SYGADYKRTYKVNAPYKINQRIIVD---PVTSEHETLCOAE-GYPAKE 164
DB 120 VQVCKERGTYGVKHLALVKLSIKADFSPN---ITSGNSADTKRTCTCAGSGFPKPR 175
QY 165 VITVSSDHOVLSCGTTTNSKREKLENTVSTLKITNTTNEIFCTRRRLDPEENHAE 224
DB 176 FSWLENGRE-LPGINTTISQDESELYTISQDLPNTTNTIKCLKYGDA---HVSDE 231
QY 225 VIPELPLAHPEERTHLVILGAILLCGVALTFI 258
DB 232 FTWEKPPEDPPDSKNTLVFGA---GFGAVITTV 262

RESULT 7
US-09-159-135-4
Sequence 4: Application US/09159135
Patent No. 6149905
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Gilmer, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells with Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B lymphocyte activation antigen; Ig
DESCRIPTION: superfamily member; T cell costimulatory signal
DESCRIPTION: via activation of CD28 pathways, binds to CD28+
DESCRIPTION: T cells, transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -37 to -1
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 210
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 211 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular (cytoplasmic) domain
LOCATION: 236 to 269
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 105
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 106 to 199
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: GRAY, GARY S.
AUTHORS: GIMMI, CLAUDE D.
AUTHORS: LOMBARD, DAVID B.
AUTHORS: ZHOU, LIANG-JI
AUTHORS: WHITE, MICHAEL
AUTHORS: FINGEROTH, JOYCE D.
AUTHORS: GRIBBEN, JOHN G.
AUTHORS: NADLER, LEE M.
TITLE: Structure, Expression, and T Cell Costimulatory
TITLE: Activity Of The Murine Homologue Of The Human B
JOURNAL: Journal of Experimental Medicine
VOLUME:
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ISSUE:
PAGES:
DATE: IN PRESS
RELEVANT RESIDUES IN SEQ ID NO: 4: From -37 to 269
US-09-139-135-4

Query Match 11.7%; Score 177.5; DB 4; Length 306;
Best Local Similarity 26.6%; Pred. No. 4.2e-10;
Matches 57; Conservative 36; Mismatches 92; Indels 29; Gaps 11;

QY 55 YVEMEDKNIQFVGEEDLVKVOHSSYRQARLKDQSLGNAALQITPVKQDAGVYRC 114
DB 68 IYQKHDKVLSVIAK--LKV-WPEYKRT--LYDNFTY---SLIIIGLVISDRCTYSC 119
QY 115 MI-----SYGADYKRITVKNAPYKRNQILVVD---PVTSEHETQAE-GYPRAE 164
DB 120 VQKKRGTYGVKHLALVLSIKADFSPN---ITSGNPADTKRITCFASGCFPKPR 175
QY 165 VMTSSDHQVLSGKTTTTSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENTAE 224
DB 176 FSWLENGRE-LPGINTTISQDEPESELYTTSQLDPTTNNHTIKLIKYGDA---HVSSED 231
QY 225 VIPELPPLAHPNERTHLVILGAILLCLGVALTFI 258
DB 232 FTWEKPEDEPPDSKNTLVLFGA---GFGAVITIV 262

RESULT 8
US-08-147-772-2

Sequence 2, Application US/08147772
Patent No. 5858776

GENERAL INFORMATION:

APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,772

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand

DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

FEATURE:

NAME/KEY: signal sequence

LOCATION: -34 to -1

IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein

OTHER INFORMATION: hydrophobic

FEATURE:

NAME/KEY: extracellular domain

LOCATION: 1 to 208

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: transmembrane domain

LOCATION: 209 to 235

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: intracellular domain

LOCATION: 236 to 254

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 19 to 21

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 55 to 57

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 152 to 154

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 177 to 179

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 192 to 194

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig V-set domain

LOCATION: 1 to 104

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202


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1 REGISTRATION NUMBER: 36, 207
2 REFERENCE/DOCKET NUMBER: RPI-004
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (617) 227-7400
5 TELEFAX: (617) 227-5941
6 INFORMATION FOR SEQ ID NO: 21:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 288 amino acids
9 TYPE: amino acid
10 TOPOLOGY: linear
11 MOLECULE TYPE: protein
12 DESCRIPTION: B cell activation antigen; natural ligand
13 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
14 FEATURE:
15 NAME/KEY: signal sequence
16 LOCATION: -34 to -1
17 IDENTIFICATION METHOD: amino terminal sequencing of
18 IDENTIFICATION METHOD: soluble protein
19 OTHER INFORMATION: hydrophobic
20 FEATURE:
21 NAME/KEY: extracellular domain
22 LOCATION: 1 to 208
23 IDENTIFICATION METHOD: similarity with known
24 IDENTIFICATION METHOD: sequence
25 FEATURE:
26 NAME/KEY: transmembrane domain
27 LOCATION: 209 to 235
28 IDENTIFICATION METHOD: similarity with known
29 IDENTIFICATION METHOD: sequence
30 FEATURE:
31 NAME/KEY: intracellular domain
32 LOCATION: 236 to 254
33 IDENTIFICATION METHOD: similarity with known
34 IDENTIFICATION METHOD: sequence
35 FEATURE:
36 NAME/KEY: N-linked glycosylation
37 LOCATION: 19 to 21
38 IDENTIFICATION METHOD: similarity with known
39 IDENTIFICATION METHOD: sequence
40 FEATURE:
41 NAME/KEY: N-linked glycosylation
42 LOCATION: 55 to 57
43 IDENTIFICATION METHOD: similarity with known
44 IDENTIFICATION METHOD: sequence
45 FEATURE:
46 NAME/KEY: N-linked glycosylation
47 LOCATION: 64 to 66
48 IDENTIFICATION METHOD: similarity with known
49 IDENTIFICATION METHOD: sequence
50 FEATURE:
51 NAME/KEY: N-linked glycosylation
52 LOCATION: 152 to 154
53 IDENTIFICATION METHOD: similarity with known
54 IDENTIFICATION METHOD: sequence
55 FEATURE:
56 NAME/KEY: N-linked glycosylation
57 LOCATION: 173 to 175
58 IDENTIFICATION METHOD: similarity with known
59 IDENTIFICATION METHOD: sequence
60 FEATURE:
61 NAME/KEY: N-linked glycosylation
62 LOCATION: 177 to 179
63 IDENTIFICATION METHOD: similarity with known
64 IDENTIFICATION METHOD: sequence
65 FEATURE:
66 NAME/KEY: N-linked glycosylation
67 LOCATION: 192 to 194
68 IDENTIFICATION METHOD: similarity with known
69 IDENTIFICATION METHOD: sequence
70 NAME/KEY: N-linked glycosylation
71 LOCATION: 198 to 200
72 IDENTIFICATION METHOD: similarity with known

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FEATURE: IDENTIFICATION METHOD: sequence
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic T Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 6
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262
US-08-101-624-23

Query Match          11.4%; Score 172; DB 2; Length 288;
Best Local Similarity 22.1%; Pred. No. 1.4e-09;
Matches 58: Conservative 56; Mismatches 97; Indels 52; Gaps 12;

25 KDLVVEGSMNTTICKRPFVERKOLALAIYWEMEDKNIIQFVGHEEDLKVOSSYHOR 84
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
43 KEVALISCGHNVSE-----ELAQTRITYOKEKKMVLTMSCDMMINTEYNN----- 89
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
85 ARLKDQLSLGNALQITDVKLQDAGYRCMI-STGGADYKR-----IIVKANAPYNK 136
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
90 -RTIPD--ITNNLSIVIALRPDSDEGTVCVLAKYEKDAFKREHLAEVTLSYKADFPPPS 146
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
137 INORLIVDPATYSHELTCQAE-GYKRAEVITWSSDHQVLSCKPTTTSKSREKLFNVS 195
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
147 ISDFE---PTSNIIRITICSTSGCPPEHLISLENGEE-LNAINTTVSJDIFTELAVSS 202
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
196 TLRIINTTNEIFYC-----TFRRRLPEENHTAELVIPELPLAHPPERTHALVL 244
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
203 KLDFWMNTTNHSFMCILIKYGLLRVNQTFFMMWNTTKQHHPDNLLPSVAI-----I, TLISVN 255
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
245 GAILLCLGVALLFTF-RUKGR 265
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
256 GIEVIC---CLTYCAPRCRERR 275

RESULT 11
US-08-751-767A-6
Sequence 6, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
U-751-767A-6

Query Match 11.48; Score 172; DB 2; Length 288;
Best Local Similarity 22.18; Pred. No. 1,4e-09;
Matches 58; Conservative 56; Mismatches 97; Indels 52; Gaps 12;

QY 25 KDLVVEGSGMTIECKFPVEKQDLALIVYMEEDKNITQFVHGEEDLKVOHSSYRQR 84
DB 43 KEVATLSCGHVSVSE-----ELAOTRIYQKREKKMVTLMSSGDMINPEKRN----- 89
QY 85 ARLLKDLQSLGNAALQITDVKLQDAGYRCMI-SYGGADYKR-----ITVKNVAPYK 136
DB 90 -RTTFD--ITNNLSIVILALRPSDEGTVECVLKEKDAFKREHLAEVTLVKADPTPS 146
QY 137 INQILLVADPTSHSLTLCQAE-GYKRAEYIWTSSDHQVLSGKTTTNSKREKLEFNTS 195
DB 147 ISDEIT--PISNIRRIICSTSGGPEPHLSWLENGEE-LNAINTVVSODEPTELYAVSS 202
QY 196 TLRINTTNEIFYC-----TFRRLDPENNHTAEIVPELPLAHPPNERTHVL 244
DB 203 KLDPMNTNHSFMCILIKHGLRVNQTFFMWNTKQEHFNDNLPSMAI-----TLISVN 255
QY 245 GAILLCGLVALTFIF--RLRGR 265
DB 256 GIFVIC--CLTYCFAPRCRERR 275

R-12
US-09-153-262-2
Sequence 2, Application US/08153262
Patent No. 6071716
GENERAL INFORMATION:
APPLICANT: FREEDMAN, GORDON J.
APPLICANT: FREEDMAN, ARNOLD S.
APPLICANT: NADLER, LEE M.
TITLE OF INVENTION: DNA Encoding B7, A New Member
TITLE OF INVENTION: Of The IgG Superfamily with Unique Expression On
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30
OPERATING SYSTEM: MS/DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,262
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 35 to 37
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:

NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: SEGILL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-153-262-2

Query Match 11.4%; Score 172; DB 3; Length 288;
Best Local Similarity 22.1%; Pred. No. 1.4e-09;
Matches 58; Conservative 56; Mismatches 97; Indels 52; Gaps 12;

QY 25 KDLYVEVGSNNTICKPEVKQDLALIVYEMEDKNIIOFVHGEDLKVOHSSYROR 84
DB 43 KEVALTSCGHNVSE-----ELAQTRIRYQKEKKMVLTMMSGDMNIMPEYKN---- 89
QY 85 ARLLKDOJSLGNAALQITDVKLDAGVYRCMT-SYGGADYKR-----ITKVNAPYRK 136
DB 90 -RTIPD--ITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADFPPTS 146
QY 137 INORILVVDPVSEHELTQOAE-GYKPAEVIWTSSDHQVLSGKTTTNSKREELFNVT 195
DB 147 ISDFEIR---PNSNIRRIITSGSGFPEHLISWLENGEE-LNAINTTVSODPTELTAVSS 202
QY 196 TLRINTTNEIFYC-----TFRRLDPEENHTAEVLPELPLAHPNERHVLVL 244
DB 203 KIDFNMNTNHSFMCILKYGHLELVNQTFFNMNTYKQEHFPDNLPSVAL-----TLISVN 255
QY 245 GAILLCGLVALFTF--RLRKGR 265
DB 256 GLEFVIC---CLTYCFAPRCRERR 275

RESULT 13
US-08-479-744A-29
Sequence 29, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation

LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 196 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-479-744A-29

Query Match 11.4% Score 172; DB 3; Length 288;
Best Local Similarity 22.1%; Pred. No. 1.4e-09;
Matches 58; Conservative 56; Mismatches 97; Indels 52; Gaps 12;

QY 25 KDLVVEGSMTECKFPYKQDLALVYMEEDKNITQFVHGEEDLKVOHSYROR 84
DB 43 KEVATLSCGHVSE-----ELQTRIVYWKCKRMVLTMMSGDMNIPVYKN--- 89
QY 85 ARLKPOLSLGNALQITDVYKLDAGVRCMT-SYGGADYR-----ITVKVAPYKN 136
DB 90 -RTIFD--ITNLSIVILALRPSDEGTIECVLYTEKDAFRREHLAEVTLVSKADFP 146
QY 137 INQRIILVDPVTSSEHETLQAE-GYKRAEVIWTSDDHQLVSGKTTTNSKREKLFN 195
DB 147 ISDEI---PTSNIRIRICSTSGGFPEPHLSMLENGEE-LNAITVTYSQDETELAV 202
QY 196 TLRINTTNEIFC-----TTRRLDPEENHTAELVIPLEPLAHAPNERTHLVIL 244

DB 203 KLDFNMTNHSFMCILIRYGLRVNQTENWMTTKOEHPDNLPSMAI---TLLSVN 255
QY 245 GAILLCIGVALTFIF--RLRGR 265
DB 256 GIVVIC--CLTYCFAPRCRRR 275

RESULT 14
US-08-280-757B-29
Sequence 29, Application US/08280757B
Patent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: NO. 6130316e1 CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known

NAME/KEY:	signal sequence
LOCATION:	-34 to -1
IDENTIFICATION METHOD:	amino terminal sequencing of
IDENTIFICATION METHOD:	soluble protein
OTHER INFORMATION:	hydrophobic
NAME/KEY:	extracellular domain
LOCATION:	1 to 208
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	transmembrane domain
LOCATION:	209 to 235
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	intracellular domain
LOCATION:	236 to 254
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	19 to 21
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	55 to 57
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	64 to 66
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	152 to 154
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	173 to 175
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	177 to 179
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	192 to 194
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	N-linked glycosylation
LOCATION:	198 to 200
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	Ig V-set domain
LOCATION:	1 to 104
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
FEATURE:	
NAME/KEY:	Ig C-set domain
LOCATION:	105 to 202
IDENTIFICATION METHOD:	similarity with known
IDENTIFICATION METHOD:	sequence
PUBLICATION INFORMATION:	
AUTHORS:	FREEMAN, GORDON J.
AUTHORS:	FREEDMAN, ARNOLD S.

1. AUTHORS: SEGIL, JEFFREY M.
 2. AUTHORS: LEE, GRACE
 3. AUTHORS: WHITMAN, JAMES F.
 4. AUTHORS: NADLER, LEE M.
 5. TITLE: 87, A New Member Of The Ig Superfamily With
 6. TITLE: Unique Expression On Activated And Neoplastic B Cells
 7. JOURNAL: The Journal of Immunology
 8. VOLUME: 143
 9. ISSUE: 8
 10. PAGES: 2714-2722
 11. DATE: 15-OCT-1989
 12. RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 13. US-09-159-135-2

[illegible]

Search completed: March 18, 2002, 06:35:53
Job time: 130 sec

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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:33:43 ; Search time 37.45 Seconds
(without alignments)
589.870 Million cell updates/sec

Title: US-09-649-108-1

Perfect score: 1511

Sequence: 1 MRFVAFIMTYMHLNAFT.....KCGIDOTNSKQSDTHLEET 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

T number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR-68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	12.2	487	2 S65133	butyrophilin - mou
2	174	11.5	526	2 A37821	butyrophilin - bov
3	172	11.4	288	2 A45803	B-cell-restricted
4	169.5	11.2	309	2 I49503	B-lymphocyte activ
5	169	11.2	526	2 S70587	butyrophilin precu
6	165	10.9	289	2 G00031	B7 protein - red-c
7	162	10.7	299	2 I46690	CD80 precursor - r
8	161.5	10.7	329	1 A48754	B7-2 antigen - hum
9	161	10.7	330	2 I46691	CD86 precursor - r
10	156	10.3	321	2 I54766	B-lymphocyte activ
11	134	8.9	391	2 T09058	butyrophilin homol
12	132	8.7	853	1 IJBONC	neural cell adhesi
13	130	8.6	1088	1 IJXJNL	neural cell adhesi
14	129	8.5	725	2 JE0099	neural cell adhesi
15	128	8.5	725	2 JE0100	neural cell adhesi
16	128	8.5	1092	1 JN0635	neural cell adhesi
17	127.5	8.4	309	2 I49522	gene B7-2 protein
18	126	8.3	1106	1 PFHUGB	platelet-derived g
19	126	8.3	5175	2 T20992	hypothetical prote
20	126	8.3	5198	2 T43290	hemiscentin precurs
21	122	8.1	761	2 IJHUNG	neural cell adhesi
22	122	8.1	1028	2 A53449	plasmacytoma-assoc
23	121.5	8.0	1338	2 S09982	protein-tyrosine k
24	120.5	8.0	646	2 I38042	cell surface glyco
25	118.5	7.8	587	2 JH0464	DM-GRASP precursor
26	118.5	7.8	588	2 JH0506	adhesion molecule
27	118	7.8	725	1 IJMSNG	neural cell adhesi
28	118	7.8	1115	1 IJMSNL	neural cell adhesi
29	117.5	7.8	2132	1 A55182	agrecan precursor

30	117	7.7	1091	1 IJCHNL	neural cell adhesi
31	116.5	7.7	243	2 I51746	myeloid class II alpha
32	116.5	7.7	370	2 S29139	agrecan - pig (fr
33	116.5	7.7	588	2 A45254	surface glycoprote
34	116.5	7.7	1427	2 I51669	tyrosine suppressor
35	115.5	7.6	333	2 A31923	adhesion protein pr
36	115	7.6	946	1 A47299	myeloid tyrosine kin
37	115	7.6	1336	2 I60598	myeloid tyrosine kin
38	114.5	7.6	2415	1 A39086	neural precursor
39	114	7.5	818	2 IJ9120	hypothetical prote
40	114	7.5	858	1 IJRTNC	neural cell adhesi
41	113	7.5	1033	2 S19247	cell adhesion prot
42	112.5	7.4	7962	2 I38346	elastic titlin - hu
43	112	7.4	1028	2 I58164	Big-1 protein - ra
44	111.5	7.4	538	2 JC2457	vascular cell adhe
45	111.5	7.4	1018	2 JC4211	neural adhesion pr

ALIGNMENTS

RESULT 1
S65133
butyrophilin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C/Accession: S65133
R:Rishii, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 285-292, 1995
A:Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically assoc
A:Reference number: S65133; MUID:96125722
A:Accession: S65133
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-487 <ISH>
A:Cross-references: GB:S80642; NID:g1246078; PIDN:AAB35893.1; QID:g1246079

Query Match 12.2% Score 185; DB 2; Length 147;
Best Local Similarity 25.7%; Pred. No. 6e-07;
Matches 62; Conservative 45; Mismatches 120; Indels 14; Gaps 6;

QY	38	IECKPVEKQLDLALVYEMEDKNIIOFVHGEEDLPKVOHSSYRCRAVLKDOISLQNA	97
DB	12	LTCGSPNASSFYMELMFRQTRSTAVLIXRGQDEGQMTREGRATLALAGLIDGRA	71
QY	98	ALQITDVKLQDAGVYRCMISYGADYKRTYKVNAPYKINQRIILVDPVTSHELTQQA	157
DB	72	TLIRIDVRFSDQGEYRCLFK-DNDPFEFAVYLKVAAGSDPOISMTVOEMCMELECTS	130
QY	158	EG-YKAEVYMTSSDHOVLSGKTTTNSKR--EKKLFNTSLKRLNITTNELFYCTFRRL	214
DB	131	SCWYEPQVQWRTGNREML---PSTSDSKKHNEEGLEFVAVSMISDSSIN--MSCCIONI	187
QY	215	DEEHNFAELVPEPLAPHPNERHVLIGAILLCLIGV---ACFTFPLP NGRMDVVK	270
DB	168	LLGQCKEVDI---SLPAPVPRLTFPIYAVATILALGLTLGSIFFTKWKLKYEKSSLRK	244
QY	271	K 271	
DB	245	K 245	

RESULT 2
A37821
butyrophilin - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C/Accession: A37821
R:Jack, L.J.W.; Mather, I.H.
J. Biol. Chem. 265, 14481-14486, 1990
A:Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycopr

A:Reference number: A37821; MUID:90354441
A:Accession: A37821
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-526 <JAC>
A:Cross-references: GB:M5551; MID:g1763685; PIDN:AAB39766.1; PID:g162773
C:Keywords: Transmembrane protein

Query Match	11.5%	Score 174;	DB 2;	length 526;
Best Local Similarity	23.6%	Pred. No.	4.8e-06;	
Matches 69;	Conservative 57;	Mismatches 144;	Indels 22;	Gaps 9;

```

Oy      6 VEIETNYHLLNA-FETVVPDOLVVEGSESMTECFKPEPKODILALIVYEMEDKNI 64
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      15 IFILLQPKRDSAPPDVGPEPILAVAGDEALPCR--LSPNVSAGMELRMFRREKVSF 72

Oy      65 IOFV--HGEEDLKVOHSSYRORARLLKQDLSLGNALQITDVKLDQAGVRCMI SYGAD 122
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dt      73 AVFVSREGQEOEGEBMEYRGVSLVEBHIEGVSVAARIVGKRSDDGEYCFEFRQ--DEN 131

Oy      123 YKRITVKVNAVDPYKINQRIILVDPDVTSEHLELTOAEG-YDKAEVYIMSDHOLSKGTT 181
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      132 YEALVHLKVAALSDPSPIISKVQESGEIQECTSVGNTPEPQOMHTHNGEEPSPSES 191

Oy      182 TNSKREELFNVTSLRIINTTNEIFYCTERRLDPEENHTAELVPELPAHPRNEKTHL 241
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      192 RNPD-EEGLFTVVRASVIIRDSMKMNVSCCINILLQGEKDEV---SIPASFPLRTPM 247

Oy      242 VILGAILLCGV----ATTFIFRLKRGMDVKYKKGCIQDINSKQSDTHLEE 289
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 VAVAVIIVLQDLITGTSLEFWRLYKEHSR-----QRRRESSKKLLLE 292

```

RESULT 3

A45803

B-cell-restricted antigen B7 precursor - human

N.Alternate names: B-lymphocyte activation antigen B7

C.Species: Homo sapiens (man)

C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999

C.Accession: U54495; A45803

C.Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.

C.Immunogenetics 35: 175-181, 1992

A.Title: Genomic organization and chromosomal location of the human gene encoding the B

A.Reference numbers: U54495; MUID:92307753

A.Accession: U54495

A.Status: translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Molecule type: DNA

A.Accession: U54495

A.Cross-references: GB:M3077; NID:g179327; PIDN:AAA58390.1; PID:g179329

R.Fireman, G.J.; Freedman, A.S.; Segill, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.

J.Immunol. 143, 2714-2722, 1989

A.Title: B7, a new member of the Ig superfamily with unique expression on activated and

A.Reference number: A45803; MUID:90010147

A.Accession: A45803

A.Molecule type: mRNA

A.Residues: 1-288 <FR>

A.Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916

C.Genetics:

A.Gene: GDB:CD80; CD28LG1; CD28

A.Cross-references: GDB:251792; OMIM:112203

A.Map position: 3q13.3-3q21

A.Introns: 34/1; 140/1; 234/1; 266/1

C.Superfamily: B-lymphocyte restricted antigen B7

C.Keywords: transmembrane protein

C.F1-26/Domain: signal sequence #status predicted <SIG>

C.F1-248-254/Domain: transmembrane #status predicted <TM>

Query Match	11.4%	Score 172;	DB 2;	Length 288;
Best Local	22.1%;	Pred. No. 3.2e-06;		
Matches	51;	Conservative	56;	Mismatches 97;
				Indels 52;
				Gaps 12;

```

OY      25 KDVVVEGSMWTECKRPPEKODLALVYMEMEDKNIIOFHGHEEDLKVHSSV ROR 84
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      43 KEVATLSGHNVAE-----ELAQTRITWKEKEMVLTMSGDMNIWPEK N--- 89
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      85 ARLLKDQSLGMAALQITVYKLODAGVYRCMI-SYGADYK R-----ITVKNVAPYK 136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      90 -RTIFD--ITNNLSVILALPSEDEGTVECVLTYEKDAFERELLAEVLTSLVKADPPTPS 146
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      137 INQRLVADPVTSEHELTQCAE-CYPAEAVIWTSSDQVOLSCKTTTNSKREELFWPTS 195
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      147 ISDFEI--PISNIRRIICSTSGGFPPEHLSWLENGEE-LNAINITVVSQDETELVAVSS 2020
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      196 TLRITNTTNEIFYC-----TERRLDPEENHTAEVLPELPLAHPNERTHLVIL 244
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      203 KLDFMWTNNSHFMCLIKYGLRVNQTFEMNTTKQEHPPNDLPLSMAY-----TLLSYN 2555
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      245 GAILLCGLVALTFIF--RLRGR 265
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      256 GIEVYC--CLTYCAPRCRERR 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 4
149503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text-change 29-Sep-1999
C:Accession: 149503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: 149503; MUID:93307789
A:Accession: 149503
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:I12589; NID:g293299; PIDN:AA037240.1; PID:g293301
R:Freeman, G.J.; Gray, G.S.; Gilmml, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fling
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homol
A:Reference number: S17291; MUID:91341422
A:Accession: S17291
A:Molecule type: mRNA
A:Residues: 1-274, 'R', 279-309 <FRE>
A:Cross-references: EMBL:X60958; NID:g50111; PIDN:CA043291.1; PID:g50112
R:Rothe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A:Title: Identification of an alternatively spliced form of the murine homologue of B
A:Reference number: 149521; MUID:94220123
A:Accession: 149521
A:Status: translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-143, 238-274, 'R', 279-309 <RE2>
A:Cross-references: GB:D16220; NID:g505118; PIDN:BA003748.1; PID:g994769
C:Genetics:
A:Gene: B7
A:Introns: 37/1, 143/1, 237/1, 275/1
C:Superfamily: B-lymphocyte restricted antigen B7
C:Keywords: alternative splicing

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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:35:58 ; Search time 25.77 Seconds
(without alignments)
412.604 Million cell updates/sec

Title: US-09-649-108-1

Sequence: 1 MRIFAVFIMTYHLLNFT.....KCGIDPTNSKQSDTHLEET 290

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 100059 seqs, 36664827 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	210	13.9	524 1	BUTY_MOUSE
2	174	11.5	526 1	BUTY_BOVIN
3	172	11.4	288 1	CD80_HUMAN
4	169.5	11.2	306 1	CD80_MOUSE
5	169	11.2	526 1	BUTY_HUMAN
6	165	10.9	322 1	ICOL_MOUSE
7	162	10.7	299 1	CD80_RABIT
8	161.5	10.7	329 1	CD86_HUMAN
9	161	10.7	330 1	CD86_RABIT
10	153.5	10.2	302 1	ICOL_HUMAN
11	139.5	9.2	319 1	A33_HUMAN
12	137	9.1	365 1	CD80_HUMAN
13	134.5	8.9	298 1	VEJA_HUMAN
14	132	8.7	853 1	NCAL_BOVIN
15	130	8.6	1088 1	NCAL_XENLA
16	128	8.5	1092 1	NCAL_XENLA
17	127.5	8.4	309 1	CD86_MOUSE
18	126	8.3	1106 1	CD86_MOUSE
19	122	8.1	321 1	TCB_FTV
20	122	8.1	761 1	NCAL_HUMAN
21	122	8.1	848 1	NCAL_HUMAN
22	121.5	8.0	1338 1	VGRI_HUMAN
23	120.5	8.0	646 1	MO18_HUMAN
24	120	7.9	365 1	CD80_MOUSE
25	119.5	7.9	349 1	ICOL_MOUSE
26	119.5	7.9	2333 1	PCGA_SCHAM
27	118.5	7.8	588 1	PCGA_CANFA
28	118	7.8	725 1	NCAL_MOUSE
29	118	7.8	1115 1	NCAL_MOUSE
30	117.5	7.8	359 1	LACH_DROME
31	117.5	7.8	2132 1	PCGA_MOUSE
32	115.5	7.6	333 1	AMAL_DROME
33	115	7.6	299 1	JAM1_HUMAN

34	115	7.6	1091 1	NCAL_CHICK	p1590 gallus gall
35	115	7.6	1336 1	VGRI_RAT	p53767 rattus norv
36	114.5	7.6	2415 1	PCGA_HUMAN	p11112 homo sapien
37	114	7.5	588 1	NCAL_RAT	p13596 rattus norv
38	111	7.3	583 1	C166_HUMAN	Q1740 homo sapien
39	111	7.3	583 1	C166_MOUSE	Q1740 homo sapien
40	110.5	7.3	2124 1	PCGA_RAT	p07897 rattus norv
41	110.5	7.3	2364 1	PCGA_BOVIN	p13608 bos taurus
42	110	7.3	626 1	MAG_RAT	p07722 rattus norv
43	109.5	7.2	274 1	OX2G_HUMAN	p41217 homo sapien
44	109	7.2	626 1	MAG_HUMAN	p20916 homo sapien
45	109	7.2	1443 1	NEOL_CHICK	Q09610 gallus gall

ALIGNMENTS

```
RESULT 1
BUTY_MOUSE STANDARD: PRT: 524 AA.
AC Q62556: P97392;
BT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
CN BTN1A1 OR BTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RA MEDLINE=97148936; PubMed=8995761;
RX Ogg S.L., Komaragiri M.V.S., Mather I.H.;
RT "Structural organization and mammary-specific expression of the
RT butyrophilin gene."
RL Mamm. Genome 7:900-905(1996).
RN [2]
RP SEQUENCE OF 39-487 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96125722; PubMed=8541302;
RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura K., Matsuda T.;
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
RT specifically associates with a 150-kDa protein of mammary epithelial
RT cells and milk fat globule membrane."
RL Biochim. Biophys. Acta 1245:285-292(1995).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC -!- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
CC PREGNANCY AND IS MAXIMAL DURING LACTATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 1
CC V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PH-PROTEIN (RFP).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U67065; AAB51034.1; -
DR EMBL: S80642; AAB35893.1; -
DR MGD: MGI:103118; Btlna1.
DR Interpro: IPR003879; Butyroph.DUF_C.
```


Db 15 IFILLQPKLDSAPFDYIGQEPILLAVGEDALPCR--LSPNVSAKGMELRFRKVP 72
 Oy 65 IOEFV--HGEEDLKQVSHSSRYORARLLKDLQSLGNAALQITVKLQDAGVRCMISYGGAD 122
 Db 73 AVFYSRGGQDEGEEMAEYKRRVSLVEDHIAEGSVAVRIQVKASDCEYCFRQ--DEN 131
 Oy 123 YKRITVKNVAPYKNIORILLVDPVTSSEHETLQAEQ-YPKAEVITWSSDHQVLSGKTTY 181
 Db 132 YEELAVHLKVAALGSDPHISMVKVQESGEIOLECTSVGMYPEPOVQWRTHREEPSPMS 191
 Oy 182 TNSRREKRLNVTSLKNTNTNTEIFCTFRRLDPEENHTALVPELPLAHPNERHIL 241
 Db 192 RNDP-EGELFLVRAVYIIRSSMKNVSCCINLLGQEKVEV---SLPASFPLTPWM 247
 Oy 242 VIICAILLCIGV---ALTFIFRLKRCMMDVKKGIQDTSKKQSDPHEE 289
 Db 248 VAVAVILVIGLITIGSIFFTWRLTKERSR-----QRNRFSSKELLEE 292
 RE T 3
 C HUMAN STANDARD; PRT; 288 AA.
 I CD80, HUMAN
 AC P33681;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1
 DE ANTIGEN (CTLA-4 COUNTER-RECEPTOR B7.1) (B7) (BBI).
 CN CD80 OR CD28LG1 OR CD28LG OR LAB7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lymphoid.
 RX MEDLINE=90010147; PubMed=2794510;
 RA Freeman G.J., Freedman A.S., Segall J.M., Lee G., Whitman J.F.,
 RA Nadler L.M.;
 RT "B7, a new member of the Ig superfamily with unique expression on
 RT activated and neoplastic B cells.";
 RL J. Immunol. 143:2714-2722(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92307753; PubMed=1377173;
 RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
 RA Dupont B.;
 RT "Genomic organization and chromosomal location of the human gene
 RT encoding the B-lymphocyte activation antigen B7.";
 RL Immunogenetics 36:175-181(1992).
 RN [3]
 RP SEQUENCE OF 35-38.
 RX MEDLINE=91341422; PubMed=1714935;
 RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
 RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
 RT "Structure, expression, and T cell costimulatory activity of the
 RT murine homologue of the human B lymphocyte activation antigen B7.";
 RL J. Exp. Med. 174:625-631(1991).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
 CC AND DENDRITIC CELLS.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD80 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".
 CC -----
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 CC -----
 DR EMBL: M27533; AAA56045.1; -
 DR EMBL: M83077; AAA58390.1; -
 DR EMBL: M83072; AAA58390.1; JOINED.
 DR EMBL: M83073; AAA58390.1; JOINED.
 DR EMBL: M83074; AAA58390.1; JOINED.
 DR PIR: A45803; A45803.
 DR MIM: 112203; -
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003600; IG_LIKE.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00409; IG_1.
 DR SMART: SM00410; IG_LIKE_1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 34
 FT CHAIN 1 288
 FT DOMAIN 35 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 288
 FT DOMAIN 43 123
 FT DOMAIN 155 223
 FT DISULFID 50 116
 FT DISULFID 162 216
 FT CARBOHYD 53 53
 FT CARBOHYD 89 98
 FT CARBOHYD 98 98
 FT CARBOHYD 186 186
 FT CARBOHYD 207 207
 FT CARBOHYD 211 211
 FT CARBOHYD 226 226
 FT CARBOHYD 232 232
 SQ SEQUENCE 288 AA; 33048 MW; BA453BE34528B1F4 CRC64;
 Query Match 11.4%; Score 172; DB 1; Length 288;
 Best Local Similarity 22.1%; Pred. No. 8.7e-08;
 Matches 58; Conservative 56; Mismatches 97; Indels 52; Gaps 12;
 Oy 25 KDLYVEYGSNMVTECKRPEVKQDLALIVWEMEDNIIOFVGEDDKAKQHSYROR 84
 Db 43 KEVATLSGCHNVSV-----ELAQTRITWQEKKNVLTMSGDHNIWPEYKN---- 89
 Oy 85 ARLKDLQSLGNAALQITVDKLDAGVRCMI-SVGADYKR-----ITVKNVAPYK 136
 Db 90 -RTIFD--ITNNLSVILALRPSDGEYECVYLKTEKAKFKHEHLAEVTLASKAPFP 146
 Oy 137 INQRLVDPVTSSEHETLQAE-QPKAEVITWSSDHQVLSGKTTYINSKREKLENVTS 195
 Db 147 ISDEFI---PTSNIRRIICSTSGEPPEHLVLENGEE-LNAINTVSDODETELAVSS 202
 Oy 196 TLRIITNTNEIFYC-----TFPRRLDPEENHTALVPELPLAHPNERHIVIL 244
 Db 203 KLDFEMTINHSPMCLIKGHLRVNQTFFMNTTKQHPDNLIPSWAI-----TLISVN 255
 Oy 245 GAILLCGLVALTFIF-RLRGR 265
 Db 256 GIFVIC---CLTYCAPRCREKR 275

RESULT	4			
ID	CD80_MOUSE	STANDARD:	PRT:	306 AA.
AC	000609;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1 ANTIGEN) (B7).			
CN	CD80 OR B7.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=91341422; PubMed=1714935;			
RA	Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,			
RA	White M., Fingerhuth J.D., Grubben J.G., Nader L.M.,			
RT	Structure, expression, and T cell costimulatory activity of the			
RT	murine homologue of the human B lymphocyte activation antigen B7.;			
RL	J. Exp. Med. 174:625-631(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=93307789; PubMed=7686531;			
RA	Selvakumar A., White P.C., Dupont B.;			
RT	Genomic organization of the mouse B-lymphocyte activation antigen			
RT	B7.;			
RL	Immunogenetics 38:292-295(1993).			
CC	-1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T			
CC	LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE			
CC	PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS			
CC	RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA			
CC	INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL			
CC	MALIGNANCIES.			
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-			
CC	ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND			
CC	IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS			
CC	ONE C2-LIKE AND ONE V-LIKE DOMAINS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X60958; CAA43291.1; -;			
DR	EMBL; L12589; AAA37240.1; ALT_SEQ.			
DR	EMBL; L12585; AAA37240.1; JOINED.			
DR	EMBL; L12586; AAA37240.1; JOINED.			
DR	EMBL; L12587; AAA37240.1; JOINED.			
DR	EMBL; L12588; AAA37240.1; JOINED.			
DR	PIR; S17291; S17291.			
DR	MGD; MGI:101775; Gdb80.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003600; Ig_Like.			
DR	Pfam; PF00047; Ig_2.			
DR	SMART; SM00409; Ig_1.			
DR	SMART; SM00410; Ig_Like; 1.			
RV	Immunoglobulin domain; T-cell; glycoprotein; signal; Transmembrane;			
RV	Receptor.			
FT	SIGNAL	1	37	
FT	CHAIN	38	306	T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT	DOMAIN	38	246	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	247	268	POTENTIAL.

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB 261
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CC -----

DR EMBL: U39576; AAC50489.1; -

DR MIM: 601610; -

DR InterPro: IPR003879; Butyrophil_DUF_C.

DR InterPro: IPR001870; Gamma_carboxylase.

DR InterPro: IPR003066; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR InterPro: IPR003877; SPRY.

DR Pfam: PF00047; 19; 1.

DR Pfam: PF00622; SPRY; 1.

DR SMART: SM00406; IGV; 1.

DR SMART: SM00449; SPRY; 1.

DR Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.

KM SIGNAL 1 26

FT CHAIN 27 526

FT DOMAIN 27 242 BUTYROPHILIN.

FT TRANSMEM 243 269 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 270 526 POTENTIAL.

F CARBOHYD 55 55 CYTOPLASMIC (POTENTIAL).

F CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 526 AA; 59004 MW; ESECA0CF8DAF94D5 CRC64;

Query Match 11.2%; Score 169; DB 1; Length 526;

Best Local Similarity 25.2%; Pred. No. 3.6e-07;

Matches 64; Conservative 44; Mismatches 132; Indels 14; Gaps 7;

QY 19 FTVTPKDLVYVEXGSMNTECKPEVEKQDLALIVYWEDEKNIIOFVH--GREDLKV 76

DB 29 FDIVGPEPIALVAVGDEALPCR--LSPNASAEHLELRFKPKVSPALVHRDGEQAE 86

QY 77 QHSYRQARALLKQSLSGNALQITDVYKQDAGYRCMISYGCADYRITYKVAAPLNK 136

DB 87 QMPEYRGATLVQDGIAGVALRIGVAVSDGEYTCFFREDGS--YEALVHLKVAALG 145

QY 137 INORILVDPVTSSEHETLCOAEG--YPKAEVMTSSDHQVLGSKTTTTSKREKLFNTS 195

DB 146 SDPHSMQVQNGECLCLECTSVGWTPPEQOVQWRTSKGKFP--STSEKNNPDEEGIFTYAA 204

QY 196 TLRINTTNEIFYCTFRRLDPEENHTALVPELPAPNPERHTLVLGAILLCGLV-- 253

DB 205 SVIIRDSTKNVSCYIOWLLGQEKVEISIPASL--PLRLPWIVAVVAVILMWGLLT 261

QY 254 --ALTFIFRLAKGR 265

DB 262 IGSIFFTWRLYNER 275

RESULT 6

ICOL_MOUSE STANDARD: PRT: 322 AA.

AC Q9JHJ8; 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50)

DE (B7-RELATED PROTEIN-1) (B7RP-1) (LICOS).

GN ICOSL OR B7H2 OR B7RP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.

RC TISSUE=Lymphocytes;

RX PubMed=10617205;

RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J., Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A., Brankov D., Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S., Hui A., McCabe S.M., Scully S., Shalinian A., Shaklee C.L., Van G., Mak T.W., Senaldi G.;

RT "T-cell co-stimulation through B7RP-1 and ICOS." Nature 400:827-832(1999).

RL Nature 400:827-832(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Thymus;

RX PubMed=10549624;

RA Swallow M.M., Wallin J.J., Sha M.C.;

RT "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by TNFalpha." Immunol 11:423-432(1999).

RL Immunol 11:423-432(1999).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=C3H/HeJ; TISSUE=fetal thymus;

RX MEDLINE=20126021; PubMed=10657606;

RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A., Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S., Jacobs K.A., Collins M.;

RT "Identification of GL50, a novel B7-like protein that functionally binds to ICOS receptor." J. Immunol. 164:1653-1657(2000).

RL J. Immunol. 164:1653-1657(2000).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Peripheral blood lymphocytes;

RX MEDLINE=21286479; PubMed=11390480;

RA Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.;

RT "Differential expression of inducible costimulator-1 ligand splice variants: lymphoid regulation of mouse g150-b and human g150 molecules." J. Immunol. 166:7300-7308(2001).

RL J. Immunol. 166:7300-7308(2001).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RA Ling V., Dunussi-Joannopoulos K.;

RT "g150 molecules and uses thereof." Patent number WO0121796, 29-MAR-2001.

RL Patent number WO0121796, 29-MAR-2001.

CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE TH2 PHENOTYPE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: 1 (SHOWN HERE) AND 2/B; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES (PARTICULARLY IN THE CORTX AND IN BOTH PRIMARY AND SECONDARY FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG, SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.

CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYOS; IN THE YOLK SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT 14.5 DPC.

CC -1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG SUBFAMILY.

CC -----

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CC EMBL: AF216747; AAF45149.1; -

DR EMBL: AF199027; AAF34738.1; -
DR EMBL: AX100591; CAC36463.1; -
DR EMBL: AX100593; CAC36464.1; -
DR EMBL: AF394451; AAK77544.1; -
DR MGI:1354701; Icos1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003606; Ig_MHC.
DR Pfam: PFO0047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00410; Ig_Like; 1.
KW B-cell activation; Immune response; Glycoprotein;
KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW Alternative splicing.
FT CHAIN 1 46
FT DOMAIN 47 322
FT TRANSMEM 278 298
FT DOMAIN 299 322
FT DOMAIN 55 145
FT DOMAIN 178 250
FT DOMAIN 31 38
FT DOMAIN 289 292
FT DISULFID 62 138
FT DISULFID 185 243
FT CARBOHYD 71 71
FT CARBOHYD 120 120
FT CARBOHYD 163 163
FT CARBOHYD 200 200
FT CARBOHYD 213 213
FT CARBOHYD 252 252
FT CARBOHYD 265 265
FT VARSPLIC 321 322
FT CONFLICT 237 237
FT SEQUENCE 322 AA; 35960 MW; 55CCBAAD12E47B6 CRC64;
Query Match 10.9%; Score 165; DB 1; Length 322;
Best local Similarity 23.8%; Pred. No. 4.1e-07;
Matches 56; Conservative 37; Mismatches 100; Indels 42; Gaps 8;
OY 33 GSNMTECKRPVEKQDLALIVYWEDEKNI--IOFVGEEDLKVOHSSYROR 89
DB 55 GSNVSLSCIDPHRRHFLSLCYVWQIENPEVSATYVLPKSPGINDV-SSYKRGHLSL 113
OY 90 DQSLGNAALQITDVKLODAGYRCMISYGADYKRITVYNAFYKINRIILVDPVTS 149
DB 114 DSKKQGNFSLKLVNPDQDEFTGRVFMNATE--LVKILEEYVLRVAANSTFVYS 170
OY 150 -----EHELTCQAE-GYPAEVIWTSDDHQLSGKTTTNSKREEK--LEFVNSTL 197
DB 171 TSDSNNGOERTYTCMSKNKYPEPNLWIMTDSLIDFALQNTVYLNKLGIDVISTL 230
OY 198 RINTTNEIFYCFRRLL-----DPEENTALL--VIPLE 229
DB 231 RLPMTSKGVLLCCVENVALHONITSSISOAESFTGNNKNTKQDETHNELKVLVPL 285
RESULT 7
CD80_RABIT STANDARD; PRT; 299 AA.
AC P42070;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1
DE ANTIGEN).
GN CD80.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B/J X CHB:HM;
RX MEDLINE=95369849; Pubmed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules."
RL Immunogenetics 42:217-220(1995).
CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb.sib.ch).
DR EMBL: D49843; BAA08643.1; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003606; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PFO0047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00410; Ig_Like; 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 32
FT CHAIN 33 299
FT DOMAIN 33 243
FT TRANSMEM 244 264
FT DOMAIN 265 299
FT DOMAIN 42 122
FT DOMAIN 154 222
FT DISULFID 49 115
FT DISULFID 161 215
FT CARBOHYD 52 52
FT CARBOHYD 88 88
FT CARBOHYD 97 97
FT CARBOHYD 122 122
FT CARBOHYD 185 185
FT CARBOHYD 206 206
FT CARBOHYD 210 210
FT SEQUENCE 299 AA; 33513 MW; 67442235CC91DE0 CRC64;
Query Match 10.7%; Score 162; DB 1; Length 299;
Best local Similarity 19.6%; Pred. No. 6.8e-07;
Matches 52; Conservative 59; Mismatches 100; Indels 54; Gaps 12;
OY 25 KDLYVEGSGNMTECKRPVEKQDLALIVYWEDEKNIIOFVGEEDLKVOHSSYROR 84
DB 42 KEMALSCDYNISID-----ELARMRYMOKDOOVMYLSISGOVAVPEKKN----- 88
OY 85 ARLLKQDLSGNALQITDVKLODAGYRCMISYG-ADYKR-----ITVYNAFYNK 136
DB 89 -RFFPD--IINNSLMLTALRLSDKGYTTCVOKNENGSPREHLTVSTLSIRADFPVPS 145
OY 137 INCRILVDPVTSHELTCQAE-GYPAEVIWTSDDHQLSGKTTTNSKREEKLFVNTS 195
DB 146 ITD---IGHDPNKKRIRCSASGSGFPEPRLLAW-MEDDEELNVAVTYVDQDLPTFLYSVSS 201
OY 196 TLRINTTNEIFYCFRRLLDPEENHTAELVIPLE-----PLAMPNERT-----H 240
DB 202 ELDFENVNHNHSYVCLIK-----YGLSVSQIFFPMSKPQEPPIQLPHVITLIVSGA 253
OY 241 LVILGAILLGLGVALTFIFRLRGR 265

Db 254 LVLAVALYCL-ACRHVARKRTR 276

RESULT 8

ID CD86_HUMAN STANDARD: PRT: 329 AA.

AC P42081: 013655; (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2

ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).

GN CD86 OR CD281G2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RF SEQUENCE FROM N.A. Pubmed=7694363;

RA Freeman G.J., Gribben J.G., Bousiotis V.A., Ng J.W.,

RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;

RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T

RT cell proliferation.";

RL Science 262:909-911(1993).

RP [2]

RF SEQUENCE OF 7-329 FROM N.A. Pubmed=7694153;

RA Akuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,

RA Lanier L.L., Somoza C.;

RT "B70 antigen is a second ligand for CTLA-4 and CD28.";

RL Nature 366:76-79(1993).

RN [3]

RF SEQUENCE OF 7-329 FROM N.A. Pubmed=7541777;

RA MEDLINE=95331831; Pubmed=7541777;

RA Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,

RA Green N.R., Gray G.S.;

RT "Genomic organization of the gene coding for the costimulatory human

RT B-lymphocyte antigen B7-2 (CD86).";

RL Immunogenetics 42:85-89(1995).

RN [4]

RF CHARACTERIZATION.

RA MEDLINE=95088403; Pubmed=7527824;

RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,

RA Okumura K., Ito D., Akuma M.;

RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T

RT cell proliferation, cytokine production, and generation of CTL.";

RL J. Immunol. 154:97-105(1995).

RN [5]

RF IDENTIFICATION AS CD86.

RA MEDLINE=94348060; Pubmed=7520767;

RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,

RA Nadler L.M., Wakasa H., Tedder T.F.;

RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and

RT activated B lymphocytes is the CD86 differentiation antigen.";

RL Blood 84:1402-1407(1994).

CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL

CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY

CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY

CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS.

CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T

CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND

CC MONOCYTES.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.

CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD86 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".

CC -----

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CC -----

DR EMBL: L25259; AAA8389.1; -

DR EMBL: 004343; AAB03814.1; -

DR EMBL: 017722; AAA86473.1; -

DR EMBL: 017717; AAA86473.1; JOINED.

DR EMBL: 017718; AAA86473.1; JOINED.

DR EMBL: 017719; AAA86473.1; JOINED.

DR EMBL: 017721; AAA86473.1; JOINED.

DR MIM: 601020; -

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR SMART: SM00406; IGV. 1.

DR PROSITE: PS00290; IG_MHC; FALSE NEG.

KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

KW Receptor.

FT SIGNAL 1 23

FT CHAIN 24 329

FT DOMAIN 24 247

FT TRANSMEM 248 268

FT DOMAIN 269 329

FT DOMAIN 33 117

FT DOMAIN 149 225

FT DISULFID 40 110

FT CARBOHYD 157 218

FT CARBOHYD 37 33

FT CARBOHYD 43 47

FT CARBOHYD 135 135

FT CARBOHYD 146 146

FT CARBOHYD 154 154

FT CARBOHYD 177 177

FT CARBOHYD 192 192

FT CARBOHYD 213 213

FT CONFLICT 27 27

FT SEQUENCE 329 AA: 37696 MW: 65043826889CF7D CRC64:

Query Match 10.7%; Score 161.5; DB 1; Length 329;

Best Local Similarity 20.9%; Pred. No. 8.6e-07;

Matches 63; Conservative 68; Mismatches 129; Indels 41; Gaps 14;

QY 18 AFTVTPKDYVVEY-GSNMTIECKFVEYKQDLALVYWEDEKNITQVH-GEEDIK 75

DB 17 AFLTSGAFLKIQAYFNETADLPFCFANSQNSQLSELVYFQDOEMVLNVEYLCKEKPD 76

QY 76 VQHSYRQARLKLKQSLGNAALQITDVKLODAGVYRGMISY---GGADYKRITVKN 131

DB 77 SVHSRYMGRTSPDSQSWT---LRHNLIQIKDKGLYQCIHHKKEFTGMRIHNNSELS 131

QY 132 APYNNINRIIVVDVPTSE--HELTQCA-EGYR---KAVIVTSSDHQVLSGKTTTNSK 185

DB 132 VLANSQPIVIVISNITENVYINLQSSITNGYEPKPKMVLRLPYNSTIIEYQCIQKQSD 191

QY 186 REELFNVTSTLRI---NTTNEIFYCFRRLLDPENHTAELVTP--ELPLAHPNERT 239

DB 192 NTELYDVISISVSFPDVTSMNITFCIL-----ETDKRLLSSPFSILNHPOPPD-- 244

QY 240 HL-----VILGAILLGLVALTFIFR-LRGRMADVYKKCI-----QDINSKQSPFHE 288

DB 245 HLPWITAVLPVITICVWVFCILIMKKKKRRPNRSYKGTNTMTREESQTKREKRIHP 304

QY 289 E 289

DB 305 E 305

RESULT 9

CD86_RABIT

ID CD86_RABIT STANDARD: PRT: 330 AA.
AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 DE ANTIGEN).
GN CD86.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J X CHBB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules."
RT Immunogenetics 42:217-220(1995).
CC 1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY BINDING CD28 OR CTLA-4, MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC 2- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC 3- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: DA9842; BAA08642.1; -
DR InterPro: IPR003006; IG_MHC.
DR SMART: IPR003596; IG_v.
DR SMART: SMO0406; IGV: 1
DR PROSITE: PS00290; IG_MHC: 1.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 330 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 149 225 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 218 POTENTIAL.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 330 AA; 37142 MW; 935CDD65C57E3EB1 CRC64;

Query Match 10.7% Score 161. DB 1; Length 330;
Best Local Similarity 23.3% Pred. No. 9.5e-07;
Matches 67; Conservative 52; Mismatches 117; Indels 52; Gaps 12;

OY 32 YGSMTTECKFPPEKODLALAIYVEMEDKNIT-QFVHGGEEDKVOHSSYRQARLLKD 90
DB 32 FNTADLPQCFPTNSQSHSLSELYFWQDERLYLYELFLGRE--KPDVNPDKYIGRTISFD 89

OY 91 QLSGNALQITDYKLODAGVYRCMISYGADYKRITPVKNAPYKINORTIIVDPVT-- 148
DB 90 QESNN--LQJHNVQIKRGVYGCFFVHHRGA-----KGLVPLVONMSLSVLANPFR 139
OY 149 -----SEHELTQCA-EGYPAKEVITWSSDHOVLSCRTTYY--NSKREKLPNVT 194
DB 140 EITLISNITRNSAINLTCSSVQGYPEPKMF-----VLKTEMTTEVDYIEKSDQNV 194
OY 195 SLTKINTY-----TNEIFCYFRRLDPEENHTALVLPRLNHPNERTHL----- 241
DB 195 GLYNISISGSLTFESDDIRNATIVCY--LQTESLETYSQHPFYPADVPYKRLMTAA 251
OY 242 VILGAILLCGLGVALTFIFRLKRGMDYKCGIDDTNSKQSDTHLEE 289
DB 252 VALTLIVCGVLFELTLMKRRKKEQDPGYCEC--ETIKKDKAKENHVEE 297
RESULT 10
ICOL_HUMAN STANDARD: PRT: 302 AA.
ID ICOL_HUMAN
AC 075144; Q9NR01; Q9HD18;
DT 15-JUL-1999 (Rel. 38, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50)
DE (B7-RELATED PROTEIN-1) (B7RP-1).
GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Carnivora; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Dendritic cell;
RX PubMed11023515;
RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds ICOS."
RT Blood 96:2808-2813(2000).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Peripheral blood lymphocytes;
RX PubMed11007762;
RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K., Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H., Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT "Characterization of a new human B7-related protein: B7RP-1 is the ligand to the co-stimulatory protein ICOS."
RT Int. Immunol. 12:1439-1447(2000).
RL [3]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Fimerty H.F., Bean K.M., Spaulding V., Fouser L.A., Leonard J.P., Hunter S.E., Zolnier R., Thomas J.L., Miyashiro J.S., Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-1-like protein that functionally binds to ICOS receptor."
RL J. Immunol. 164:1653-1657(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."
RL DNA Res. 5:169-176(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Ling V., Dunnst-Joannopoulos K.;
RT "GL50 molecule and uses therefor."

```

CC Patent number W00121796, 29-MAR-2001.
CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: 1 (SHOWN HERE) AND 2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
CC LYMPH NODES, LEUKOCYTES AND SPLEEN.
CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC -1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 300
CC ONWARD FOR AN UNKNOWN REASON.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF199028; AAC34739.1; -
DR EMBL; AF289028; AAC01176.1; -
DR EMBL; AF216749; AAK16241.1; -
DR EMBL; AB014553; BAA31628.1; ALT_SEQ.
DR EMBL; AX100595; CAC36465.1; -
DR MIM; 605717; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 1.
DR KW B-cell activation; Immune response; Glycoprotein;
DR Immunoglobulin domain; Signal; Transmembrane; Multigene family;
DR KW Alternative splicing.
FT SIGNAL 1
FT CHAIN 19 302 POTENTIAL.
FT DOMAIN 19 256 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 257 277 CYTOPLASMIC.
FT DOMAIN 278 302 POTENTIAL.
FT DOMAIN 30 120 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 151 223 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 37 113 POTENTIAL.
FT DISULFID 158 216 POTENTIAL.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 300 302 GHV -> ESMNLLILDS (IN ISOFORM 2).
SO SEQUENCE 302 AA; 33349 MW; 647934E21B55E34A CMC64;

Query Match 10.2%; Score 153.5; DB 1; Length 302;
Best Local Similarity 22.7%; Pred. No. 3.8e-06;
Matches 60; Conservative 46; Mismatches 111; Indels 47; Gaps 9;
07 33 GSNMTIECKPPEKQDLALALVYVMEEDKNIIQVHGEGEDLAKVQH--SSYQQRARLLKD 90
08 30 GSDVELSCACPEGSGRSLNDVYVWQTSKTVYTHIIPQNSLEVDVSRNALMSFA 89

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Oy 91 OLSGNALQITDVKDAGVYRCMI-----SVGGADYKRITVK-----VANAPNK 136
Db 90 GMLRDEFSRLRENTPEQDOKFHLVLSQSIGFQVLSVEVTLHAANFSVH VVSAPHS- 148
Oy 137 INORLLVDPVTSSEHLTQCA-EGYKPAKEVMTSSD-----HOVLSGKTTTNSKREBK 190
Db 149 -----PSDELTFCTSGINGRPBNVYWKNTDSSLDOALQNDIVFLNMR---GL 196
Oy 191 ENVSTLAINTTNTTIEFCTPRRLDPEENHRA-----ELVYIPELPLAHPNNEETH 240
Db 197 YDVSVSLRIARPPSVNICCIENVLQGNLTGVSGQTGNDIGERDKITENPVSTGEKNAT 256
Oy 241 LVIIIG-AIILCLGVALTFIFELR 262
Db 257 WSLIHLVCLLVVANAIGWVCDR 280

RESULT 11
A33_HUMAN
ID A33_HUMAN STANDARD: PRT: 319 AA.
AC 099795:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33).
GN GPa33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homi.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RP TISSUE=Colon carcinoma;
RC MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.W., Rilter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN [2]
POST-TRANSLATIONAL MODIFICATIONS.
RP MEDLINE=97396159; PubMed=9245713;
RA Rilter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium."
RL Blochem. Biophys. Res. Commun. 236:682-686(1997).
CC -I- FUNCTION: MAY PLAY A ROLE IN CELL-CELL RECOGNITION AND SIGNALING.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN NORMAL GASTROINTESTINAL
CC EPITHELIUM AND IN 95% OF COLON CANCERS.
CC -I- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 K D-N-LINKED
CC CARBOHYDRATE.
CC -I- PTM: PALMITOYLATED.
CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -----
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CC -----
DR EMBL: U79725; AAC50957.1;
DR HSPB; P06907; INED.
DR MIM: 602171;
DR InterPro: IPR003006; Ig_MHC.

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DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_Like; 1.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319
FT DOMAIN 22 235
FT TRANSMEM 236 256
FT DOMAIN 257 319
FT DOMAIN 36 124
FT DOMAIN 139 229
FT DOMAIN 258 261
FT DISULFID 43 117
FT DISULFID 162 211
FT DISULFID 146 222
FT CARBOHYD 112 112
FT CARBOHYD 200 200
FT CARBOHYD 223 223
SS SEQUENCE 319 AA; 35632 MW; 9BFC7A9F45C2408E CRC64;
Query Match 9.28; Score 139.5; DB 1; Length 319;
Best Local Similarity 22.08; Pred. No. 6,7e-05;
Matches 58; Conservative 47; Mismatches 106; Indels 53; Gaps 11;
OY 16 LNAFTVVPKDLVVEGSMNTTECKFPVEK-----QDLAL-----IVYEMEDKN 63
DB 19 VDAISVETPODVLARASGSKSTLPCTYHTSTSSREGLIOMDKLLTTERVYVMPFSKN 78
OY 64 IIOFAGEEDLKVQSHSSRQARLLKDLQSLGN-----ALQITDVKLDAGYRCMIS 117
DB 79 ---YIHE-----LYKNRVSISNNAEQSDASITIDQLTMADNGYECVS 120
OY 118 -----YGAADKRTIVKVNAPYKINORLVDPYTSHELTQCA-EGYKAEVITWSSDH 172
DB 121 LMSDLENTSRVRLVLPSPKCEGIEGTIGNMQLTQCKSESPPYQYSW--KRY 178
OY 173 QVLSGKTTTNSKREKLEFNTSTLRINTTNEIFCYGFRLDPEE--NHTAEVILPELP 230
DB 179 NILNDEPPLAQPASGVY-----SLKNISTDTISGYICTSSNEGTQRCNITVAVRPSMN 234
OY 231 LA---HPNERTHLVILGAILLC 250
DB 235 VALYVGIAVGVALIITIGIITTC 258
R 12
CXAR_HUMAN STANDARD; PRT; 365 AA.
ID P78310; 000694;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR PRECURSOR (COXSACKIEVIRUS B-
ADENOVIRUS RECEPTOR) (HCAR) (CVB3 BINDING PROTEIN).
GN CXADR OR CAR.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97191019; Pubmed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Kitchin A., Hong J.S., Horvitz M.S., Crowell R.L., Finberg R.W.,
RT Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5.
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE=97250541; Pubmed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20008750; Pubmed=10543405;
RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RA Bowles N.E.;
RT "Genomic organization and chromosomal localization of the human
RT coxsackievirus B-adenovirus receptor gene";
RL Hum. Genet. 105:354-359(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Anderson C.W., Kleczawa J., Dunn J.J., Fretwell P.;
RT "Sequence and expression of CXADR, the human gene for the
RT coxsackievirus and adenovirus receptor";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL: U07593; CA68868.1; -;
DR EMBL: U90716; AAC51234.1; -;
DR EMBL: AF169366; AAF05908.1; -;
DR EMBL: AF169366; AAF05908.1; JOINED.
DR EMBL: AF169361; AAF05908.1; JOINED.
DR EMBL: AF169362; AAF05908.1; JOINED.
DR EMBL: AF169363; AAF05908.1; JOINED.
DR EMBL: AF169364; AAF05908.1; JOINED.
DR EMBL: AF169365; AAF05908.1; JOINED.
DR EMBL: AF200465; AAF24344.1; -;
DR MIM: 602621; -;
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00410; IGV; 1.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT DOMAIN 238 258
FT TRANSMEM 259 365
FT DOMAIN 34 127
FT DOMAIN 135 219
FT DOMAIN 155 210
FT DISULFID 162 212
FT DISULFID 106 106
FT CARBOHYD 201 201
SS SEQUENCE 365 AA; 40029 MW; AB01C6346CBFB64 CRC64;
Query Match 9.18; Score 137; DB 1; Length 365;
Best Local Similarity 21.58; Pred. No. 0.00013;
Matches 58; Conservative 47; Mismatches 119; Indels 46; Gaps 9;
OY 18 AFTVVPKDLVVEGSMNTTECKFPVEKQDLALIVY-----EMEDKNIIQVYHG 70
DB 19 SLSTTPEEMIEKAKGETAYLPCKFTLSPE-DQGPLDIEMILSPADNOKVDQVILLY-SG 76
OY 71 EEDLKVQSHSSRQARLLKDLQSLGNALQITDVKLDAGYRCMISYGAADYKRTIVKV 130

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Db 77 DKIVDDYDPDLKGRVHFTSNLDKSGDASINVTNLQSLDIGYQAVK-----KA 125
Qy 131 NAFPNKINQRLIYNDP-----VTSHELTQCAEGYPRKAEVITWSDHOVLGSK 178
Db 126 PGVANKKITHLVVLPKSPARCVDGSEIGSDFKIKCE---PKGSLPLOYEOKLSDS 181
Qy 179 TTTNSKREKLEFNTSTLRTINTTNEIFYCFERLDPDENHTALVPELPAPNMR 238
Db 182 QKMPSTMLAEHTSSVYSIKNASSEYSGTYCTVRNRKVSDDCLLNLNV-----PPSK 235
Qy 239 THLVILGAI---LLCLGVALTFIFRLRKR 265
Db 236 AGL-IAGAIIGTLALALIGLIIFCRCRKR 264

RESULT 13
VEJA_HUMAN STANDARD; PRT; 298 AA.
ID VEJA_HUMAN
P57087;
1 20-AUG-2001 (Rel. 40, Created)
2 20-AUG-2001 (Rel. 40, Last sequence update)
3 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED MOLECULE PRECURSOR (VE-JAM).
GN C2I0RF43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular endothelial cells;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.C., Hammerich S., Rosen S.D.;
RT "Vascular endothelial junction-associated molecule, a novel member of
RT the immunoglobulin superfamily," is localized to intercellular
RL J. Biol. Chem. 275:19139-19145(2000).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC SECONDARY LYMPHOID ORGANS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC
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CC
DR EMBL: AF255910; AAF81223.1;
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003600; IG_Like.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00410; IG_Like; 1.
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 20
FT CHAIN 21 298
FT
FT DOMAIN 21 238 VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED
FT TRANSMEM 239 259 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 260 298 POTENTIAL.
FT DOMAIN 43 116 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 148 221 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 50 109 IG-LIKE C2-TYPE DOMAIN.
FT

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FT DISULFID 155 214 POTENTIAL.
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 298 AA; 33207 MW; CA7B518E22DCAAE CRC64;

Query Match 8.9%; Score 134.5; DB 1; Length 298;
Best Local Similarity 21.4%; Pred. No. 0.00017;
Matches 65; Conservative 52; Mismatches 112; Indels 75; Gaps 16;

Qy 18 AFTVYVPKDLVY---VEGSSNMTIECKFP---VEKQDLAALIVWEMEDKNIQFVHGE 71
Db 26 AYGFSAKPKQGVVTAVER-QEALIACTPKTKTVSSRL-----WKRIAGRS-VSPVYVQ 76
Qy 72 EDLKVQHSYRQPARILKQSLGNALDITPVKLDQADGVYRCHMSYSGADYKRITVKYN 131
Db 77 QTLQ---GDFKNRAEMI-----DFNIRIKKVTNRSDACKYRCILVSAPEOQO-----N 120
Qy 132 APYNNKINQRLIYNDPVTSEH-----ELTQO-AEGYPRKAEVITWSDHOVLGSKT 179
Db 121 LEDVTYTLLEVLAAPVAPSCVPSSALSGTVVELRCDKQKGNPAPEYTWKKGDIRLENPR 180
Qy 180 TTTNSKREKLEFNV-TSTLRINTTT-----NEIFY--CFIRLDPDENHTAL 224
Db 181 LGSQSTNSSTYMTNTKGTGLQFMTVSKLDGEGYSCLEARNSVGRKRCGRMVDLINSIGI 240
Qy 225 VIPELPLAHPNDRTHLVILGAILLCLGVALTFIFRLRGRMIDVKKCIOTNSKQSD 284
Db 241 I-----AAVVVAIVSVGLGV--CYAQRKGYES--KETSFOKSNSSSKAT 283
Qy 285 THLE 288
Db 284 TMSF 287

RESULT 14
NCAL_BOVIN STANDARD; PRT; 853 AA.
ID NCAL_BOVIN
P31836;
1 01-JUL-1993 (Rel. 26, Created)
2 01-JUL-1993 (Rel. 26, Last sequence update)
3 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain cortex;
RX MEDLINE=89378239; PubMed=2776887;
RA Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V.,
RA Petukhova G.V., Raktina T.V., Feshchenko E.A., Ishchenko K.A.,
RA Mitroeva S.F., Chernova M.N., Dranitsyna S.M.;
RT "Calmodulin-independent bovine brain adenylate cyclase. Amino acid
RT sequence and nucleotide sequence of the corresponding cDNA."
RT FEBS Lett. 254:69-73(1989).
RN 12
RP SEQUENCE OF 20-36.
RX MEDLINE=86140120; PubMed=3512556;
RA Rougon G., Marshak D.R.;
RT "Structural and immunological characterization of the amino-terminal
RT domain of mammalian neural cell adhesion molecules."
RL J. Biol. Chem. 261:3396-3401(1986).
RN 13
RP IDENTIFICATION AS N-CAM.
RX MEDLINE=92111748; PubMed=1765159;
RA Premont R.T.;
RT "A bovine brain cDNA purported to encode calmodulin-insensitive

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RT adenylyl cyclase has extensive identity with neural cell adhesion
RL molecules (N-CAMs).
CC FBS Lett. 295:230-231(1991).
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC NEURITES, ETC.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A CALMODULIN-
CC INDEPENDENT ADENYLATE CYCLASE.
CC -----
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CC -----
DR EMBL: X16451; CAA34470.1; -.
DR PIR: A32976; IJBNC.
DR HSSP: P40189; 1BQU.
DR InterPro: IPR001777; FN_III.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00408; IgC2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT CHAIN 1 19
FT 20 853 NEURAL CELL ADHESION MOLECULE, 140 KDA
FT 20 719 ISOFORM.
FT TRANSMEM 720 737 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 738 853 POTENTIAL.
FT DOMAIN 738 853 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 132 103 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 132 196 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 228 293 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 321 401 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 428 495 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 527 604 FIBRONECTIN TYPE-III 1.
FT DOMAIN 633 700 FIBRONECTIN TYPE-III 2.
FT DOMAIN 152 156 HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 161 165 HEPARIN-BINDING (POTENTIAL).
FT DISULFID 161 165 BY SIMILARITY.
FT DISULFID 139 189 BY SIMILARITY.
FT DISULFID 235 286 BY SIMILARITY.
FT DISULFID 328 394 BY SIMILARITY.
FT CARBOHYD 435 488 BY SIMILARITY.
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 853 AA; 93893 MW; E12FD49231A7A368 CRC64;

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Query Match 8.7%; Score 132; DB 1; Length 853;
 Best Local Similarity 26.3%; Pred. No. 0.0012;
 Matches 47; Conservative 28; Mismatches 54; Indels 50; Gaps 8;

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DB 188 RCEGRIILARGEINFRDIQIVNVP-PIVQAROSIVNATANIQSIVLWCAECPPEPTVS 246
QY 167 WTSSDHQVLSGKTTTNSKREKLEFNVTSTLRIMTTNEIFCYCFRRRLDPENNTAAELV 225
DB 247 WTKGGEQI-----ENEDKYLFSDDS-----ELTIKRYD--KNDAAEYV 285
RESULT 15
NCAL XENLA STANDARD; PRT; 1088 AA.
AC P16170:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180)
DE [CONTAINS: N-CAM 140].
GN NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90098871; PubMed-2481269.
RA Kriegl P.A., Sakaguchi D.S., Kintner C.R.;
RT "Primary structure and developmental expression of a large
RT cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT molecule (NCAM).";
RL Nucleic Acids Res. 17:10321-10335(1989)
CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
CC NEURITES, ETC.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
CC TISSUE.
CC -1- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC EARLY NEURAL DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M25696; AAA49909.1; -.
DR PIR: S09600; IXLNL.
DR HSSP: P56276; 1TLK.
DR InterPro: IPR001777; FN_III.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00408; IgC2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT CHAIN 1 19
FT 20 1088 NEURAL CELL ADHESION MOLECULE 1, LARGE
FT 20 705 ISOFORM.
FT TRANSMEM 706 723 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 724 1088 POTENTIAL.
FT DOMAIN 129 193 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 225 289 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 225 289 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 225 289 IG-LIKE C2-TYPE DOMAIN 3.

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 06:35:03 ; Search time 62.55 Seconds
(without alignments)
678.161 Million cell updates/sec

Title: US-09-649-108-1

Perfect score: 1511

Sequence: 1 MRFEAFVIFMTWHLNAPF.....KCGIDPTNSKKQSDPHLEET 290

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTRMBL_17:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mmc:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1511	100.0	290	4	Q9NZ07
2	1050	69.5	290	11	Q9EP73
3	918	60.8	176	4	Q9NUZ5
4	404	26.7	273	4	Q9BQ51
5	343	22.7	247	11	Q9WUJ5
6	310	20.5	316	4	Q9BXRI
7	185	12.2	282	4	Q9H6B2
8	181.5	12.0	296	13	Q42A04
9	181	12.0	329	6	Q9TFP2
10	179	11.8	288	6	Q9TFP2
11	175	11.6	288	6	Q28499
12	174	11.5	296	6	Q46405
13	170	11.3	286	6	Q46535
14	169.5	11.2	306	11	Q9R129
15	167	11.1	526	4	Q9H458
16	165	10.9	288	6	Q9BDN6
17	165	10.9	289	6	Q28347
18	165	10.9	322	11	Q9HJ78
19	162.5	10.8	272	11	Q70356

20	162.5	10.8	321	11	Q55202	Q92 ratius norv
21	161	10.7	290	11	Q62680	Q9280 ratius norv
22	161	10.7	321	11	Q35187	Q35187 ratius norv
23	160	10.6	323	6	Q9BDM9	Q9Bdm9 macaca neme
24	159.5	10.6	326	11	Q70358	Q70358 mus musculu
25	159.5	10.6	329	6	Q9XSX6	Q9xsx6 felis silve
26	159.5	10.6	332	6	Q9GCM27	Q9gcm27 felis silve
27	156	10.3	321	11	Q62624	Q62624 ratius norv
28	154.5	10.2	280	6	Q9TFP1	Q9tfp1 canis famli
29	153.5	10.2	302	4	Q9HD18	Q9hd18 homo sapien
30	153.5	10.2	309	4	Q9NRQ1	Q9nrq1 homo sapien
31	153	10.1	323	6	Q9BDM4	Q9bdm4 macaca mula
32	150.5	10.0	323	6	Q9BDM2	Q9bdm2 cercopithec
33	150	9.9	323	6	Q9BDB8	Q9bdb8 cercocobus
34	148	9.8	292	6	Q02758	Q02758 felis silve
35	148	9.8	292	6	Q9GMD8	Q9gmd8 felis silve
36	148	9.8	325	6	Q02838	Q02838 sus scrofa
37	147.5	9.8	586	4	Q9HCY2	Q9hcy2 homo sapien
38	144	9.5	304	6	Q9TOX1	Q9tox1 canis famli
39	144	9.5	523	4	Q00480	Q00480 homo sapien
40	143.5	9.5	351	5	Q9VYO0	Q9vyo0 drosophila
41	143.5	9.5	527	4	Q00475	Q00475 homo sapien
42	143	9.5	325	11	Q70359	Q70359 mus musculu
43	140.5	9.3	529	4	P78408	P78408 homo sapien
44	139.5	9.2	284	6	Q9GL33	Q9gl33 bos taurus
45	139.5	9.2	319	11	Q9JKA5	Q9jka5 mus musculu

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	290 AA.
Q9NZ07	Q9NZ07	Q9NZ07		
AC	Q9NZ07	Q9NZ07		
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	B7-H1 (PD-1-LIGAND PRECURSOR).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20048154; PubMed=10581077;			
RA	Dong H., Zhu G., Tamada K., Chen L.;			
RT	"B7-H1, a third member of the B7 family, co-stimulates T cell			
RT	proliferation and interleukin-10 secretion.";			
RL	Nat. Med. 5:1365-1369(1999).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PLACENTA;			
RX	PubMed=11015443;			
RA	Freeman G.J., Long A.J., Iwai Y., Bourque K., Chernova T.,			
RA	Nishimura H., Fitz L., Malenkovich N., Okazaki T., Byrne M.C.,			
RA	Horton H.F., Fouser L., Carter L., Ling V., Bowman M.R., Carreno B.M.,			
RA	Collins M., Wood C.R., Honjo T.;			
RT	"Engagement of the PD-1 immunoinhibitory receptor by a novel B7-family			
RT	member leads to negative regulation of lymphocyte activation.";			
RL	J. Exp. Med. 192:1027-1034(2000).			
CC	- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN			
DR	EMBL: AF177937; AAF25807.1; -			
DR	EMBL: AF233516; AAG18508.1; -			
DR	InterPro: IPR003599; Ig			
DR	InterPro: IPR003600; Ig_Like			
DR	InterPro: IPR003006; Ig_MHC			
DR	Pfam: PF00047; Ig_2			
DR	SMART: SM00409; Ig_1			
DR	SMART: SM00410; Ig_Like; 1.			
KW	Signal.			
FT	SIGNAL	1	18	POTENTIAL.

FT CHAIN 19 290 PD-1-LIGAND.
SQ SEQUENCE 290 AA: 33275 MW: FE957086E62A31A8 CRC64:

Query Match 100.0%; Score 1511; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 2e-127;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIFAVFEMTYVHLLNFVTVPKDLVVEYSGNMTECKEPVEKQDLALIVYWEKE 60
DB 1 MRIFAVFEMTYVHLLNFVTVPKDLVVEYSGNMTECKEPVEKQDLALIVYWEKE 60
QY 61 DKNITQFVGEEDLKVOVSHSRQRRARLLKDQLSLGNALQITDVKLDQAGYRCMTISGG 120
DB 61 DKNITQFVGEEDLKVOVSHSRQRRARLLKDQLSLGNALQITDVKLDQAGYRCMTISGG 120
QY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
QY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
QY 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
DB 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
QY 241 LVITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290
DB 241 LVITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290

RESULT 2

Q9EP73 PRELIMINARY; PRT: 290 AA.
AC Q9EP73;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PD-1-LIGAND PRECURSOR (B7-H1 PROTEIN).
GN PCDD1L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX PubMed=11015443;
RA Freeman G.J., Long A.J., Iwai Y., Bourque K., Chernova T.,
RA Nishimura H., Filtz L., Malenkovich N., Okazaki T., Byrne M.C.,
RA Horton H.F., Fouser L., Carter L., Ling V., Bowman M.R., Carreno B.M.,
RA Collins M., Wood C.R., Honjo T.,
RT "Engagement of the PD-1 Immunoinhibitory receptor by a novel B7-family
RT member leads to negative regulation of lymphocyte activation.";
RL J. Exp. Med. 192:1027-1034(2000).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Tamura H., Dong H., Zhu G., Sica G.L., Flies D.B., Tamada K., Chen L.;
RT "B7-H1 costimulation preferentially enhances CD28-independent T helper
RT cell function.";
RL Blood 0:0-0(2000).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF233517; AAC18509.1; -;
DR EMBL: AF317088; AAC31810.1; -;
DR MGD: MGI:192646; Pgcd11.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00410; IG_Like; 2.
DR Signal.
FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 290 PD-1-LIGAND.
SQ SEQUENCE 290 AA: 32780 MW: AB7C46CF853EBB02 CRC64:

Query Match 69.5%; Score 1050; DB 11; Length 290;
Best Local Similarity 69.4%; Pred. No. 4e-86;
Matches 202; Conservative 34; Mismatches 53; Indels 2; Gaps 2;

QY 1 MRIFAVFEMTYVHLLNFVTVPKDLVVEYSGNMTECKEPVEKQDLALIVYWEKE 60
DB 1 MRIFAVFEMTYVHLLNFVTVPKDLVVEYSGNMTECKEPVEKQDLALIVYWEKE 60
QY 61 DKNITQFVGEEDLKVOVSHSRQRRARLLKDQLSLGNALQITDVKLDQAGYRCMTISGG 120
DB 61 DKNITQFVGEEDLKVOVSHSRQRRARLLKDQLSLGNALQITDVKLDQAGYRCMTISGG 120
QY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
QY 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
DB 121 ADYKRITVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQVSGKTT 180
QY 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
DB 181 TTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAHPPNERTH 240
QY 241 LVITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290
DB 240 WLLGSITLFLIVSTVLLFLRKQVRMLDVEKGVEDTSSKNNDTQREET 290

RESULT 3

Q9NUZ5 PRELIMINARY; PRT: 176 AA.
AC Q9NUZ5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CDNA FLJ1032 FIS, CLONE PLACE1004197, WEAKLY SIMILAR TO BUTYROPHILIN
DE PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX Isoqai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuko Y., Sasaki N.,
RT "NEDO human cDNA sequencing project.";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AK001894; BAA91966.1; -;
SQ SEQUENCE 176 AA: 19959 MW: E40B76615611F34 CRC64:

Query Match 60.8%; Score 918; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.4e-74;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 MISYGADYKRTTVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQV 174
DB 1 MISYGADYKRTTVKNVAPYKINORILVDPVTSSEHETQCAEGYPAEYIWTSSDHQV 60
QY 175 LSGKTTTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAH 234
DB 61 LSGKTTTNSKREKLFNVSTLRINTTNEIFYCTFRRLDPEENHFAELVPELPLAH 120
QY 235 PNERTHVLITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 290
DB 121 PNERTHVLITGAILLCGVALTFIFRLKRGKMDVKKCGIODTNSKKOSDTHLEET 176
RESULT 4

09B051 PRELIMINARY: PRT: 273 AA.
 ID 09B051
 AC 09B051
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE BUTYROPHELLIN PRECURSOR B7-DC (PD-1-LIGAND 2 PROTEIN).
 GN PD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tseng S.-Y., Otsuji M., Gorski K., Huang X., Slansky J.E., Pai S.I.,
 RA Shalabi A., Shin T., Pardoll D.M., Tsuchiya H.;
 RT "B7-DC, a new dendritic cell molecule with potent costimulatory
 RT properties for T-cells."
 RI J. Exp. Med. 193:839-846(2001).
 [2]
 SEQUENCE FROM N.A.
 RA Latchman Y., Wood C.R., Chernova T., Chaudhary D., Borde M.,
 RA Chernova I., Iwai Y., Long A.J., Brown J.A., Nunes R.,
 RA Greenfield E.A., Bourque K., Boussoletis V.A., Carter L.L.,
 RA Carreno B.M., Melnikovich N., Nishimura H., Okazaki T., Honjo T.,
 RA Sharpe A.H., Freeman G.J.;
 RT "PD-L2 is a second ligand for PD-1 and inhibits T cell activation."
 RT Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF329193; AAK31105.1;
 DR EMBL: AF344424; AAK15370.1;
 SO SEQUENCE 273 AA; 30897 MW; 8B7E963C8AA26EC8 CRC64;

Query Match 26.7%; Score 404; DB 4; Length 273;
 Best Local Similarity 38.1%; Pred. No. 2.8e-28;
 Matches 106; Conservative 40; Mismatches 94; Indels 38; Gaps 10;

QY 19 FTVTVPKDLVYVEGSGNMTIECKFPVEKQDLALIVWEMEDKNIQFVNEEDLKVOH 78
 DB 21 FTVTVPKDLVYVEGSGNMTIECKFPVEKQDLALIVWEMEDKNIQFVNEEDLKVOH 78
 QY 79 --SSYRQARILKQDLSGNALQITDVKLQDAGVRCMISYGA-DYKRITVKNAPYN 135
 DB 65 DTSNHRERATLLEQLPLGKASFIHQVQVRDEGQYOCIIITGVAMDVKYTLFKAKASR 124
 QY 136 KINQRIIVDPVTSSEHETLCAEGYPKAEVIWTSDDHVLGSKTTTNSKREELFNVT 195
 DB 125 KINQHILKV-PETDEVELTLCATGCPPLAEVSWPN-----VSVPANTSHSRPEGLYQVTS 178
 QY 196 TLRINTTNEIFCYGFERLDEENHTALVPELPLAHPNERTLVILGAILL--CLGV 253
 DB 179 VLRLKPPGRNPFSCVF-----WNTHVELTILASIDLOSOMEPRTHPWHLHIFISCI-I 232
 QY 254 ALRFI--FRLKGRMDVKKCGIOTNSKROSDTHLE 288
 DB 233 AFIFATVIALRK--QLCQKLYSSKMDTKRPVTTTKRE 266

RESULT 5
 ID 09B051 PRELIMINARY: PRT: 247 AA.
 AC 09B051
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE BUTYROPHELLIN-LIKE PROTEIN.
 GN BTDC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C;
 RA Tseng S., Gorski K., Huang X., Pardoll D., Tsuchiya H.;
 RT "Butyrophilin like molecule in dendritic cell."
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF142780; AAD33892.1;
 DR InterPro: IPR003599; I9_1;
 DR InterPro: IPR003600; I9_1like.
 DR InterPro: IPR003006; I9_1MHC.
 DR Pfam: PF00047; I9_2;
 DR SMART: SM00409; I9_1;
 DR SMART: SM00410; I9_1like; I9_1;
 SO SEQUENCE 247 AA; 27819 MW; 9BFDDE1AF3EC138F CRC64;

Query Match 22.7%; Score 343; DB 11; Length 247;
 Best Local Similarity 37.1%; Pred. No. 7.1e-23;
 Matches 92; Conservative 41; Mismatches 89; Indels 26; Gaps 8;

QY 19 FTVTVPKDLVYVEGSGNMTIECKFPVEKQDLALIVWEMEDKNIQFVNEEDLKVOH 78
 DB 21 FTVTVPKDLVYVEGSGNMTIECKFPVEKQDLALIVWEMEDKNIQFVNEEDLKVOH 78
 QY 79 SSYRQARILKQDLSGNALQITDVKLQDAGVRCMISYGA-DYKRITVKNAPYNKI 137
 DB 70 ---SERATLLEQLPLGKALFHIPSVQVNDSCGYRCLVTCGAMDKYTLFKAKASYMRI 126
 QY 138 NORILVDPVTSSEHETLCAEGYPKAEVIWTSDDHVLGSKTTTNSKREELFNVTSTL 197
 DB 127 DRIILEV-PGTEGVOLTCARGYPLAEVSW-----QNSVPANTSHSRPEGLYQVTSVL 180
 QY 198 RINTTNEIFCYGFERLDEENHTALVPELPLAHPNERT--KLVLGAILLCLGVA 254
 DB 181 RLKPPSRNFSQMFNAHMKELTSA--IIDPLSRMEKVPRTMPLCHVFIPACTIALIFLA 238
 QY 255 LTFIFRLR 262
 DB 239 IVTIQRRK 246

RESULT 6
 ID 09BXR1 PRELIMINARY: PRT: 316 AA.
 AC 09BXR1
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE COSTIMULATORY MOLECULE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chapoval A.I., Ni J., Lau J.S., Wilcox R.A., Flies D.B., Liu D.,
 RA Dong H., Sica G.L., Zhu G., Tamada K., Chen L.;
 RT "B7-H3: A costimulatory molecule for T cell activation and IFN-gamma
 RT production."
 RL Nat. Immun. 2:269-274(2001).
 DR EMBL: AF302102; AAK15438.1;
 SO SEQUENCE 316 AA; 33791 MW; FP97007F191CCFAL CRC64;

Query Match 20.5%; Score 310; DB 4; Length 316;
 Best Local Similarity 30.1%; Pred. No. 8.9e-20;
 Matches 85; Conservative 50; Mismatches 133; Indels 14; Gaps 5;
 QY 15 LTNATVTVPKDLVYVEGSGNMTIECKFPVEKQDLALIVWEMEDKNIQFVNEEDLKVOH 74
 DB 25 LTGALEVGVPEDPVVALVGTDAITLCCSFSPGFSIAQLNIMQLDTRK--LVHSFAG 82

RESULT	7	
CC	002	
AC	009682	PRELIMINARY;
AC	009682	PRT; 282 AA.
DT	01-MAR-2001 (TREMBLrel, 16, Created)	
DT	01-MAR-2001 (TREMBLrel, 16, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel, 17, Last annotation update)	
DE	CDNA: FLJ22418 FIS, CLONE HRC08590.	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
CX	NCBI_TaxID=9606;	

RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RT Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AK026071; BAB15349.1; -,
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00409; IG_1.
DR SMART: SM00410; IG_1like; 1.
SO SEQUENCE 282 AA; 30893 MW; 6F9066999A1E9DB4 CRC64;

Very Match	12.28	Score 185;	DB 4;	length 282;
Best Local Similarity	23.48	Pred. No. 1.2e-08;		
Matches 65; Conservative	55;	Mismatches 96;	Indels 62;	Gaps 15;

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QY      53  LIIYWEKMDKIIIOFVH-----GEEDLKVOHSTYQORARILKDLQSLCNALQITDVKLOD  108
Db      67  IVIQWLK--GVLLIYHEFEKGGKDELSEDEMFGRVAFVDFDQIVYINASIRLKNVOLTJD  124

QY     109  AGVYRCMI-----SYGADYKRITQKVAPARYKINQRLIVDPVYSEHETLCOA--EGYKPA  163
Db     125  AGYTKCIYITISKGGNANLEKKTQAFSMP--EVN-----VDYANASSETLCEAPRMFPOP  177

QY     164  EYIVTSDHOVLSCKTYTTTNSKREKLENTYSLRI-----NTTNEIEFYCTFRRLDPEE  218
Db     178  TVVNAS---QVDOGAFNSEVSNTEFELNSENVTAKVVSVLVNTYNTNTSYCMI-----E  228

QY     219  NH-----TAEIVPELPRLAHPRNESTHVIIGG-ILLLD  251
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DT	01-JAN-1998 (TEMBLrel. 05, Last sequence update)			
DT	01-JUN-2001 (TEMBLrel. 17, Last annotation update)			
DE	CB80-LIKE PROTEIN PRECURSOR.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Inteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-WHITE LEGHORN;			
RA	O'Regan M.N.;			
RL	Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.			
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: Y08823; CAA70058.1; -			
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DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig_2.			
DR	SMART: SM00409; Ig_1.			
DR	SMART: SM00410; Ig_Like; 1.			
SO	SEQUENCE 296 AA; 3315 MW; 061572PEB238CC76 CRC64;			

Query Match	12.0%	Score 181.5;	DB 13;	Length 296;
Best Local Similarity	24.8%	Pred No. 2.6e-08;		
Matches	60;	Conservative	83;	Indels 47;
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Qy	67	FVH---GEEDLKQVHSSRYORARLLKDQSLGNAALQITDVKLQICGVCYRCMI	STGCAD	122
Db	66	VVHALISGQDNESQCSQFKNRTQLDMDKLDGDDGFSLLTNVRSDENHYKQCVWVQ---	IE	124
Qy	123	YKR-----IYVKNAAYNKINQIL---	VDPYTSHELT - GQAE - GYPKAEVITSS	170
Db	125	YTRVIRHQEYVLSLAASY---	SQPIISGPIRNSYSTEEVTFCSRQNGPEPNAVIN-	180
Qy	171	DHVLGSGTKTTTNSCKREELFNV-----	STRIRNTTNEI IYCYCFRRILDPENH	220
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 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
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 GN CD86.
 OS *Canis familiaris* (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; *Canis*.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20093996; PubMed=10630300;
 RA Yang S., Slim G.-K.;

OM of: US-09-649-108-1 to: GenEmbl:* out_format: pfs
Date: Mar 18, 2002 7:26 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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gb_pat:AX088399	+	1511.00	2633.26	1.7e-138	1553	AX088399 Sequence 3 from Paten
gb_pat:AX088422	+	1511.00	2633.26	1.7e-138	1553	AX088422 Sequence 3 from Paten
gb_pat:AF233516	+	1511.00	2633.26	1.7e-138	1553	AF233516 Homo sapiens PD-1-11g
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gb_pat:BC011497	+	216.00	353.15	2.1e-11	3437	BC011497 Mus musculus, Similia
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REFERENCE

1 (bases 1 to 873)
Dong, H., Zhu, G., Tamada, K. and Chen, L.
B7-H1, a third member of the B7 family, co-stimulates T-cell proliferation and interleukin-10 secretion
Nat. Med. 5 (12), 1365-1369 (1999)

JOURNAL

MEDLINE
PUBMED
20048154
10581077

AUTHORS

2 (bases 1 to 873)
Dong, H., Zhu, G., Tamada, K. and Chen, L.
Direct Submission
Submitted (16-AUG-1999) Immunology, Mayo Clinic, 200 First Street,
SW, Rochester, MN 55905, USA

FEATURES

Location/Qualifiers

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ACCESSION AX088399
VERSION AX088399.1 GI:13397264
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Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
REFERENCE..
1 (bases 1 to 1553)
AUTHORS Wood,C. and Freeman,G.J.

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TITLE Pg 1, a receptor for b7-4, and uses therefor
JOURNAL Patent: WO 0114557-A 3 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US); GENETICS INSTITUTE, INC.
(US)
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DEFINITION Sequence 3 from Patent WO0114556.
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VERSION AX088422.1 GI:13397287
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1553)
AUTHORS Freeman, G., Bousiotis, V., Chernova, T. and Malenkovich, N.
TITLE Novel b7-4 molecules and uses therefor
JOURNAL Patent: WO 0114556-A 3 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 968)
AUTHORS Wood, C. and Freeman, G. J.
TITLE Pd-1, a receptor for b7-4, and uses therefor
JOURNAL Patent: WO 0114557-A 1 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US); GENETICS INSTITUTE, INC.
(US)

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VERSION AX088420.1 GI:13397285
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REFERENCE 1 (bases 1 to 968)
AUTHORS Freeman, G., Bouslocis, V., Chernova, T. and Malenkovich, N.
TITLE Novel b7-4 molecules and uses therefor
JOURNAL Patent: WO 0114556-A 1 01-MAR-2001;
DANA-FARBER CANCER INSTITUTE, INC. (US)

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VERSION AK001894.1 GI:7023444
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REFERENCE
1 (sites)
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugeno,S., Aotsuka,S., Yoshikawa,Y.,
Matsunaga,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuno,Y. and Sasaki,N.
NEDO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 1301)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission

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JOURNAL Submitted (16-FEB-2000) to the DDBJ/EMBL/Genbank databases. Takao
Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yama,
Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp,
Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'-6' end one pass sequencing and clone selection;
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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ACCESSION AF317088
VERSION AF317088.1 GI:11139711
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ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 873)
Tamura, H., Dong, H., Zhu, G., Sica, G. L., Files, D. B., Tamada, K. and
Chen, L.
B7-H1 costimulation preferentially enhances CD28-independent T
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2 (bases 1 to 873)
Tamura, H., Dong, H., Zhu, G., Sica, G. L., Ffiles, D. B., Tamada, K. and
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Direct Submission
Submitted (26-OCT-2000) Immunology, Mayo Clinic, 200 First Street,
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KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
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Wood, C. and Freeman, G.J.
Pd-1, a receptor for b7-4, and uses therefor
Patent: WO 0114557-A 22 01-MAR-2001;
DANA-FABER CANCER INSTITUTE, INC. (US) ; GENETICS INSTITUTE, INC.
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LOCUS AX088429 3593 bp DNA PAT 17-MAR-2001
DEFINITION Sequence 10 from Patent WO0114556.
ACCESSION AX088429
VERSION AX088429.1 GI:13397294
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 3593)
Freeman, G., Bousiolis, V., Chernova, T. and Malenkovich, N.
Novel b7-4 molecules and uses therefor
Patent: WO 0114556-A 10 01-MAR-2001;
DANA-FABER CANCER INSTITUTE, INC. (US)
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    DEFINITION Mus musculus PD-1-ligand precursor, mRNA, complete cds.
    ACCESSION AF233517
    VERSION AF233517.1 GI:10567623
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            Freeman,G.J., Long,A.J., Iwai,Y., Bourque,K., Chernova,T.,
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            Horton,B.M., Fouser,L., Carter,L., Ling,V., Bowman,M.R.,
            Carreno,B.M., Collins,M., Wood,C.R. and Honjo,T.
            Engagement of the PD-1 immunoinhibitory receptor by a novel B7
            family member leads to negative regulation of lymphocyte activation
            J Exp. Med. 192 (7), 1027-1034 (2000)
    JOURNAL
        MEDLINE
        20472788
    REFERENCE
        2 (bases 1 to 3593)
            Freeman,G.J., Long,A.J., Iwai,Y., Bourque,K., Chernova,T.,
            Nishimura,H., Fitz,L., Malenkovich,N., Okazaki,T., Byrne,M.,
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            and Honjo,T.
            Direct Submission
            Submitted (11-FEB-2000) Adult Oncology, Dana-Farber Cancer
            Institute, 44 Binney St., Boston, MA 02115, USA
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        JOURNAL
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VERSION      AX079673.1 GI:13159242
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REFERENCE
AUTHORS      Baker,K.P., Goddard,A. and Wood,W.I.
TITLE      Human polypeptides and methods for the use thereof.
JOURNAL
Genentech, Inc. (US)
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LOCUS      AC093339      215352 bp      DNA      HNG      20-AUG-2001
DEFINITION      Mus musculus clone RP23-5G6, WORKING DRAFT SEQUENCE, 10 unordered
                pieces.
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AC093339 GI:15213884
 VERSION HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 KEYWORDS house mouse.
 SOURCE Mus musculus.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 215352)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 JOURNAL Mus musculus, clone RP23-566
 REFERENCE 2 (bases 1 to 215352)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chopel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J., Dodge, S., Ferro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hages, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Labocque, K., Lamas, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Menus, L., Minova, T., Mienna, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnapp, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996, 1997)
 http://ftp.genome.washington.edu/RW/RepeatMasker.html
 COMMENT Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L13374
 Center clone name: 5.G.6
 Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 211504 bases at least Q40
 Consensus quality: 213314 bases at least Q30
 Consensus quality: 213966 bases at least Q20
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 Insert size: 214452; sum-of-coverage
 Quality coverage: 10.1 in Q20 bases; sum-of-coverage
 Quality coverage: 10.2 in Q20 bases; sum-of-coverage
 NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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 * 1966 2065: gap of 100 bp
 * 2066 2527: contig of 462 bp in length
 * 2528 2627: gap of 100 bp
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4701 4800: gap of 100 bp
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 * 7064 10441: contig of 3378 bp in length
 * 10442 10541: gap of 100 bp
 * 10542 14119: contig of 3578 bp in length
 * 14120 14219: gap of 100 bp
 * 14220 25551: contig of 11332 bp in length
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 * 25652 61039: contig of 35388 bp in length
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ACCESSION AF344424
VERSION AF344424.1 GI:13183882
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SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
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Latchman,Y., Wood,C.R., Chernova,T., Chaudhary,D., Borde,M.,
Latchman,Y., Iwai,Y., Long,A.J., Brown,J.A., Nunes,R.,
Greenfield,E.A., Bourque,K., Bousiottis,V.A., Carter,L.L.,
Carrero,B.M., Malenkovich,N., Nishimura,H., Okazaki,T., Honjo,T.,
Sharpe,A.H. and Freeman,G.J.
PD-L2 is a second ligand for PD-1 and inhibits T cell activation
Unpublished
2 (bases 1 to 1223)
Latchman,Y., Wood,C.R., Chernova,T., Chaudhary,D., Borde,M.,
Chernova,I., Iwai,Y., Long,A.J., Brown,J.A., Nunes,R.,
Greenfield,E.A., Bourque,K., Bousiottis,V.A., Carter,L.L.,
Carrero,B.M., Malenkovich,N., Nishimura,H., Okazaki,T., Honjo,T.,
Sharpe,A.H. and Freeman,G.J.
Direct Submission
Submitted (01-FEB-2001) Adult Oncology, Dana-Farber Cancer
Institute, 44 Binney St., Boston, MA 02115, USA
TITLE
JOURNAL
REFERENCE
AUTHORS
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IIVGVAMGKYILFLKVASYRKINTHILKPEDEVELCOATGYLAIVSPNNYSV
PAMNSHPEGEIVQVSVLRKPPRNFSVCVMNTHRELEITLASIDLOSOMEPRTH
PTMHLHFIETSCIAIFIAFIADVIALRQDLQKLYSSMDTTRKRPVTTTKREVNSAI"
BASE COUNT 342 a 305 c 257 g 319 t
ORIGIN
alignment_scores:
Quality: 411.50 Length: 271
Ratio: 2.286 Caps: 9
Percent Similarity: 66.421 Percent Identity: 39.114

```

```

Alignment block:
US-09-649-108-1 x AF344424
..

Align seg 1/1 to: AF344424 from: 1 to: 1223

19 PheThrValThrValProLysAspLeuValValLutryrGlySerAs
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
334 TTCACGATCACTACCTCCCTTAAGACACTGTACATATATAGACATGGCCACCA 383
35 mMetThrIleGluCysLysPheProValIleLutrySGlnLeuAspLeuAla 52
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
384 TGTGACCCCTGGATGCAACTTTGTACACTGTGAAGACATGTGAACCTTGAG 433
52 ILeuIleValIlyrTrpGlnMetClnAspLysAsnIleIleGlnPheVal 68
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
434 CATAACACCCCACTTTGCCAA..... 453
69 HISGLIGLIGLusPLeuLysValGlnHis.....SerSerTYrArgJ 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
454 .....AAGTGGAAATATGATACATCCCGCACACCGTGA 145
83 nArgAlaIArgLeuLeuLysAspClnLeuSerLeuGlyAsnAlaIalaLeuG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
486 AAGAGCCACTTGTCTGTGAGGAGCAGCGCCCTTAGGGAAGCCCTGCTTCC 535
100 IuilePheAspValLysLsleuGlnAspIlaGlyValTYrArgCysMetIle 116
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
536 ACCTTACTCAAGTCCCAAGTGAAGGAGCAGACAGCATCAATGCAATATTC 585
117 SerTYrGlyGlyAla...AspTYrLysArgIleThrValLysValAsnAl 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
586 ACTATAGGGGTGCGCTGGGACACTACAAGTACTGACTGCAAGATCAACAC 635
132 aProTYrAsnLysIleAsnGlnArgIleLeuValAlaAspProValrThrs 149
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
636 TTCTCTACAGAAATATAACCTCCATCACTCAAAAGTT...CCGAATAACAG 682
149 eGlnIuISglnLeuThrCysGlnAlaGlnGlyTYrProLysAlaGlnVal 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
683 ATGAGGTAGACATCCACTTCCGACAGCTACAGTTTCTCTGGCAGAACTA 7
166 ILeTrpThrSerSerAspHisGlnValLeuSerGlyLysThrThrThr 182
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
733 TCTGTGCCAAAC.....GTCAGCGTTCTCGCCACACACCAG 767
182 rAnSerLysArgGlnGlnLysLeuPheAsnValThrSerThrLeuArgI 199
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
768 CCACCTCAGAGACCCCTGAAGCGCTCTACACAGGTACCAGATGTTCTGCC 817
199 LeasnthrThrThrAsnGlnIlePheTYrCysThrPheArgArgLeuAsp 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
818 TTAAGCACCCCCCTGGCAGAAACTCTACGCTGTGTGTTCC..... 855
216 ProGlnGluAsnHisThrAlaGlnLeuValIleProGlnLeuProLeuAl 232
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
856 ...TGGAAATCACTACGAGGAGAACTTACTTTGGCCAGCATGTGACTTCA 902
232 aHisProProAsnGlnArgThrHisLeuValIleLeuGlnAlaIalaLeu 249
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
903 AAGTCAGATGAGACCAAGACCCATCCCAACTGGCTGCTTCCACTTTTCA 924
249 eu.....CysLeuGlnValAlaLeuThrPheIlePheArgLeuAsnLys 263
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
953 TCCCCCTCCGTCATC...ATTGCTTTCAATTTCATAGGCACACAGTGMACCC 999
264 GlyArgMetMetCAspValLysLysCysGlyIleGlnAspThrAsnSerI 280
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1000 CTAAAGAAACAACTGTCTCAAAAGCTGTATTTCTCAAAAGACACACACAA 1049
280 yLysGlnSer 283
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1050 AAGACCTGTGA 1060

```



```
129 sValasnaIaProTyraenLysIleasnGlnargIleuValaAsp 146
|||||
202 AGTCAATGCCCATACAAACAAATATCAACCAAGAAATTTGGTTGGATC 251
|||||
146 rovalThSerGlnHISgIuLeuThrCysGlnAlaGluGlyTyrProLys 162
|||||
252 CAGTCACTCTGACATGACATGACATGTGACGTGAGGGCTACCCCAAG 301
|||||
163 AlaGluValIleTrrPThrSerSerAspHisGlnValIleuSerGlyLysTh 179
|||||
302 GCGGAAGTCATCTGACAAAGCAGTGCATCAATCCAGTCCGTAGTAAGAC 351
|||||
179 rThrThrThrasenSerLysArgGluGluLysLeuPheAsnValThrSert 196
|||||
352 CACCAACCAATTCACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 401
|||||
196 hrLeuArgIleasnThrThrThrasnGluIlePheTyrCysThrPheArg 212
|||||
402 CACTGAGATCAACACAACTAATGAGATTCTTACTGCACCTTTTAAAG 451
|||||
213 ArgLeuAspProGluGluAsnHisThrAlaGluLeuValIleProGluLe 229
|||||
452 AGATTAGATTCCTGAGGAAACCATACAGTGAATGGTCATCCAGACT 501
|||||
229 uProLeuAlaHisProProAsnGluArgThrHisLeuValIleLeuGlyA 246
|||||
502 ACCTCTGGCAGATCCTCCAAATGAAGAGACTCATTGGTAATCTGGGAG 551
|||||
246 IaIleLeuLeuCysLeuGluValAlaIleLeuThrPheIlePheArgLeuArg 262
|||||
552 CCATCTTTATGCTTGCTGTACACAGTGCATCTCTCGTTTAAAGA 601
|||||
263 LysGlyArgMetMetAspValLysLysCysGlyIleGlnAspThrAsnSe 279
|||||
602 AAAGGAGAGATGATGATGTGAAAAATGTGGCATCCAAAGATACAAACTC 651
|||||
279 rLysLysGlnSerAspThrHisLeuGluGluThr 290
|||||
652 AAAGAGCAAACTGATACCATTTGGAGAGAGAGC 685
|||||

seq_name: gb_est1:AI733919
seq_documentation_block:
LOCUS AI733919 464 bp mRNA EST 24-OCT-2000
DEFINITION z150f01.y5 Soares ovary tumor NBHOT Homo sapiens cDNA clone
IMAGE:725785 5', mRNA sequence.
VERSION AI733919
VENDOR AT733919.1 GI:5055032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 464)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: z150f01.s1
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-NCI human EST project
This read has been verified (found to hit its original self in the
correct orientation)
Putative full length read
The vector to vector length is 544
Insert length: 621 Std Error: 0.00
Seq primer: -40RP from Gibco.
Location/Qualifiers

FEATURES
```

```
source
1. .464
/organism="Homo sapiens"
/db_xref="GDB:5937732"
/db_xref="taxon:9606"
/clone="IMAGE:725785"
/clone_1lb="Soares ovary tumor NBHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site: 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not 1 - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGGCGCGCGGTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not 1 and cloned into
the Not 1 and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Renato Soares and
M.Fatima Bonaldo"

BASE COUNT 145 a 108 c 105 g 106 t
ORIGIN

alignment_scores:
Quality: 726.00 Length: 140
Ratio: 5.186 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
us-09-649-108-1 x AI733919

Align seg 1/1 to: AI733919 from: 1 to: 464

88 LeuLysAspGlnLeuSerLeuGlyAsnAlaIleGlnIleThrAspVal 104
|||||
9 TTGAAGGAGACACCTCTCCCTGGAAATGCTGCATTCAGATCAGAGATG 58
|||||
104 LysLeuGlnAspAlaGlyValTyrArgCysMetIleSertYrGlyGlyA 121
|||||
59 GAAATTGAGAGATGACAGGGGTGTACCGCTGCATGATCAGTATGCTGGT 108
|||||
121 IaAspTyrLysArgIleThrValLysValAsnAlaProTyraenLysIle 137
|||||
109 CCGACTACAGCGAATTTACTGTGAAGTCATATGCCCATACAAACAAATC 158
|||||
138 AsnGlnArgIleLeuValValaAspProValThrSerGlnHisGlnLeuTh 154
|||||
159 AACCAAGAAATTTGGTGTGATCCAGTACACCTCTGAAACATGAACTGAC 208
|||||
154 rCysGlnAlaLeuGluGlyTyrProLysAlaGluValIleTrrPThrSertA 171
|||||
209 ATGTCAAGCTGAGGGCTACCCCAAGCCGAAAGTCACTGGACAAACACATG 258
|||||
171 sPHisGlnValLeuSerGlyLysThrThrThrThrThrasenSerLysArgL 187
|||||
259 ACCATCAAGTCTGTAGTGTGAAGACACACACCAATTCACAAAGAGAG 198
|||||
188 GlnLysLeuPheAsnValThrSertThrLeuArgIleAsnThrThrThrAs 204
|||||
309 GAGAGCTTTTCAATGTGACACGACACTGAGAAATCAACACAAACATVA 358
|||||
204 ngIuIlePheTyrCysThrPheArgArgLeuAspProGluGluAsnHisT 221
|||||
359 TGAGATTTTCTACTGCACTTTTAAAGAGATTGATCTTGAGGAAACATA 408
|||||
221 hrAlaGluLeuValIlePro 227
|||||
409 CAGCTGAATTTGTCATCCCA 428
|||||

seq_name: gb_est1:AA292201
seq_documentation_block:
LOCUS AA292201 497 bp mRNA EST 08-AUG-1997
DEFINITION z150f01.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone
```



```

194 huserThirleuArqIleasnTrnThrThrasuGluIlephelyrCysTr 210
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
627 ACAGGCTCTCGGCGGTGCTGGCGAATGGACACCTACAGCTCCG 676
211 pheArGArT.....LeuAspProGlu.....GluAsnH1 220
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
677 GAGCGCAATCCGCTGCTGCAGCCAGGATCGCAGCGACTCTGTACAGCATCA 726
220 sThraIaGluLeuValIlePro 227
| ||| |||||
727 CAGGCGATCGCTATGACATCC 748

seq_name: gb_est1:AL537691

seq_documentation_block:
LOCUS AL537691 857 bp mRNA EST 13-FEB-2001
DEFINITION LT1_FLO13_FBrn1 Homo sapiens cDNA clone CSODF026YL01 5
prime, mRNA sequence.
ACCESSION AL537691 GI:12801184
VERSION AL537691.1
XREF EST.
DBLINKS human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 857)
AUTHORS Li,M.B., Gruber,C., Jesssee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..857
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODF026YL01"
/clone_1kb="LT1_FLO13_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 133 a 291 c 290 g 139 t 4 others
ORIGIN

alignment_scores:
Quality: 267.50 Length: 202
Ratio: 2.140 Gaps: 4
Percent Similarity: 61.881 Percent Identity: 33.168

alignment_block:
US-09-649-108-1 x AL537691 ..

Align seg 1/1 to: AL537691 from: 1 to: 857

15 LeuLeuAsnAlaPheThrValThrValProLysAspLeuTyrValValG1 31
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
265 CTCACAGAGAGCCCTGAGAGGTCCAGGCTCGTGAAGACCCAGTGTGACCT 314
31 uTyrgIySerAsnMetThrIleGluCysLysPheProValGluLysGlnL 48
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
315 GGTGGGCGAGATGCACCCCTGTGCTGCTCTTCTCCCTGAGCCGTGCT 364

```

[illegible]

/note="Vector: PCWSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCWSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 150 a 274 c 277 g 147 t 1 others
ORIGIN

alignment_scores:
Quality: 265.00 Length: 224
Ratio: 1.893 Gaps: 6
Percent Similarity: 59.829 Percent Identity: 32.051

alignment_block:
9-649-108-1 x AL545252 ..

Align seg 1/1 to: AL545252 from: 1 to: 849

```

15 LeuLeuAaAlaPheThrValThrValProLysAspLeuTyrValValG1 31
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
128 CTCACAGAGAGCCCTGGAGGCTCCCTGACGCTCCGACAGCCAGTGGGCT 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
31 uTyrGlySerAsnMetThrIleGlyLysPheProValGluGlyGlnL 48
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178 GGTGGGACCGATGCCACCCTGCTGCTCTCTCTCCCTGAGCTGGCT 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
48 euAspLeuAlaAlaLeuIleValTyrTrpGluMetGluAspLysAsnIle 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
228 TCAGCCTGGACAGCTCAACCTCATCTGGACCTGACAGTACAA... 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 IleGlnPheValHisGlyGluGluAspLeuLysValGlnHisSerSery 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
275 ..CAGCTGGTGACACGCTTGTCTGTGAGGCCGACGAGCGGCGCCTA 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
81 rArgGlnrGAlaArgLeuLeuLysAspGlnLeuSerLeuGlnAsnAla 98
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 TGCCACGCGACAGGCCCTCTTCTGTGACCTGCTGACAGGCGACAGCAT 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
98 lAlaGlnIleThrAspValLysLeuGlnAspAlaGlyValTyrArgCys 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
372 CCCTGAGCTGCAGAGCGTGGCTTTTGGGAGCAGGCGAGCTTACCTTC 421
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
115 MetIleSerTyrGlyGlyAlaAspTyrLysArgIleThrValLysValAs 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
422 TTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGACCTGACAGTGGC 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
131 nAlaProTyrAsnLys.....IleAsnGlnArgIleL 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
472 CGCTCCCTACCTGAGGCCAGCATGACCTGACGCCCAAGGACCTGC 521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
142 euValValAspProValThrSerGlnHisGluLeuThrCysGlnAla... 157
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
522 GGCCCGGGACATGCTGAC.....ATCAGCTGCTCCAGCTAC 559
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
158 GluGlyTyrProLysAlaGluValIleThrPheSerSerAspHisGlnIva 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
560 CAGGCGTACCTGAGGCTGAGGTTCCTGCGCAGGATGGGACAGGCTGCC 609
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
174 lLeuSerGlyLysThrThrThrThrAsnSerLysArgGluGluLysLeuP 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
610 CCTGACTGGACAGTGCACAGCTCCAGATGCCACAGAGGGGCTTGT 659
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
191 heAsnValThrSerThrLeuArgIleAsnThrThrThrAsnGluIlePhe 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
660 TTGATGTGCACAGCATCTCGGGGTGTGTGGGTGCAATGGCACCTTAC 709
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
208 TyrCysThrPheArgArgLeuAspProGluLysHisThrAlaGluLe 224

```

```

710 AGCTCCGTGGCGCACCCTGCTGCTGACAGAGATGCCACAGCT..... 754
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
224 uValleProGluLeuProLeuAlaHisPro.....ProAsnGlu 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
755 .....CTGTACCATCTACACCCCGACAGACAGCCCGACGAGAC 791
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
238 rG 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
792 CG 793

```

seq_name: gb_est1:AL584057

seq_documentation_block:

```

LOCUS AL584057 683 bp mRNA EST 28-FEB-2001
DEFINITION AL584057 StrataGene Chick Embryo Lambda cDNA Library (* 937405)
ACCESSION AL584057
VERSION AL584057.1 GI:13162788
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 683)
REFERENCE
AUTHORS Murray,F.
TITLE StrataGene Chick Embryo Lambda cDNA Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
Seq primer: T3.

```

FEATURES

source

```

1..683
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS003B03"
/clone_id="StrataGene Chick Embryo Lambda cDNA Library (*
937405)"
/tissue_type="Embryo"
/dev_stage="5 days old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="vector: pBluescript SK(-) Site_1: EcoRI; Site_2: XhoI
vector. Average insert size: 1.5kb.; 5' adaptor sequence:
5' GAATTGGGACGAG 3'; 3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTTCTTTT 3'"

```

BASE COUNT 220 a 124 c 165 g 170 t 4 others
ORIGIN

alignment_scores:
Quality: 263.00 Length: 117
Ratio: 2.922 Gaps: 1
Percent Similarity: 76.923 Percent Identity: 46.154

alignment_block:
US-09-649-108-1 x AL584057 ..

Align seg 1/1 to: AL584057 from: 1 to: 683

```

110 GlValTyrArgCysMetIleSerTyrGlyGlyAlaAspTyrLysArg11 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3 GGGCTTACNATTCCTATTGAGATGGGAGCTGACTACAGNCAT 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
126 eThrValLysValAsnAlaProTyrAsnLysIleAsnGlnArgIleLeu 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 CAATCGAAAGTTCAGGCTCTTACAGACATATAACCCAGAA.....G 96

```


CC which are useful for treating immunological disorders, such as autoimmune diseases e.g., heart disease, myocardial infarction and atherosclerosis or in the case of inhibiting rejection of transplants. These fusion CC proteins are also used as immunogens to produce anti-B7-4 antibodies. CC Bp-1 is useful in promoting the maintenance of pregnancy. B7-4 protein is highly expressed in placental trophoblasts and plays a role in preventing CC maternal rejection of the foetus. B7-4 cDNA is also useful for gene mapping.

XX Sequence 1552 BP; 466 A; 312 C; 384 G; 390 T; 0 other;

alignment_scores:

Quality: 1511.00 Length: 290
Ratio: 5.210 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-649-108-1 x AAD02773 ..

seg 1/1 to: AAD02773 from: 1 to: 1552

```

1 MetAgtlIlePheAlaValPheIlePheMetHrYrTrpHisLeuLeuAs 17
|||||
53 ATGAGCATATTTGCTGCTTTATATTCATGACCTAGCTGCGCATTTCTGAA 102
|||||
17 nAlaPheThrValThrValProLysAspLeuTyValValGluTyGlys 34
|||||
103 CGCATTTACTGTCACGCGTTCCCAAGACCTATATGTGGTAGGATGGTA 152
|||||
34 eAsnMetThrIleGluCysLysPheProValGluLysGlnLeuAspLeu 50
|||||
153 GCAATATACAAATGAAATCCAGTAGAAACAAATAGACCTG 202
|||||
51 AlaAlaLeuIleValTyTrpGluMetGluAspLysAsnIleIleGlnP 67
|||||
203 GCTGCACATATTTGCTATTGGGAAATGGAGCATTAAGAACATTATTCAT 252
|||||
67 eValHisGluGluAspLeuLysValGlnHisSerSerTyArgGlnA 84
|||||
253 TGTGCATGAGAGGAAAGACCTGAAGCTTACAGATAGTACAGACAGA 302
|||||
84 rGAlaArgLeuLeuLysAspGlnLeuSerLeuGlyAsnAlaIleLeuGln 100
|||||
303 GGGCCGGCTGTGAAAGACCAAGCTCTCCGAAATGCTGCACTTCAG 352
|||||
101 IleHrAspValLysLeuGlnAspAlaGlyValTyArgCysMetIleSe 117
|||||
53 ATCACAGATGCAAAATTCAGAGATCAGGGGTGACCGCTCATGATCAG 402
|||||
117 rTyArgIlyAlaAspTyLysArgIleHrValLysValAsnAlaProT 134
|||||
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134 yTrAsnLysIleAsnGlnArgIleLeuValAlaAspProValThrSerGlu 150
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151 HisGluLeuThrCysGlnAlaGluIlyTyProLysAlaGlnValIleTr 167
|||||
503 CATGAACTGACATGTCAGGCTGAGGCTACCCCAAGCCGAAGTATCTCG 552
|||||
167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrAsnS 184
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553 GACACAGCAGTGCATCAAGTCTCAGTGGTAAGACCAACACCAACCAAT 602
|||||
184 eLysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
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603 CCAACAGAGAGAGAAAGCTTTTCATGTGACCAACACACTGAGATCAAC 652
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201 ThrThrThrAsnGluIlePheTyTrpCysThrPheArgArgLeuAspProG 217
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653 ACACACATTAATGAGATTTTCTACTGCACTTTTAGGACATTAGATCTCGA 702

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seq_name: /SIDS2/gcdata/geneseq/geneseqn/NA2001.DAT: AAD02708

seq_documentation_block:

ID AAD02708 standard; cDNA; 1553 BP.

AC AAD02708;

DT 31-MAY-2001 (first entry)

XX Human B7-4 membrane (B7-4M) protein cDNA.

XX Human; B7-4 membrane protein; B7-4M; chromosome 9; antiviral; Influenza;
KW immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;
KW graft-versus-host disease; GVHD; immunological disorder; Herpes disease;
KW autoimmune disease; common cold; shingles disease; encephalitis; therapy;
KW organ transplant; gene mapping; transgenic; viral infection; SS.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 53..925

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FT /*tag= b

FT mat_peptide 107..922

FT /*tag= c /product= "Mature human B7-4 membrane (B7-4M) protein"

XX WO200114556-A1.

XX 23-AUG-2000; 2000MO-US23256.

XX 23-AUG-1999; 99US-0150390.

XX (DAND) DANA FARBER CANCER INST INC.

XX Freeman G, Bousiotis V, Chernova T, Malenkovich N;

XX WP1: 2001-202936/20.

XX DR P-PSDB; AAY72645.

XX New human B7-4 polypeptides useful for enhancing the immune response

XX PT against a viral infection or induce a tumor immunity and to diagnose

XX PS conditions related to aberrant B7-4 expression or activity

XX Claim 1; Fig 2; 123pp; English.

XX The present cDNA sequence encodes human B7-4 membrane (B7-4M) protein

XX having a transmembrane and short cytoplasmic domain. Human B7-4 protein

CC is isolated from human activated keratinocyte and placental CDNA
CC libraries. B7-4 gene is localised on human chromosome 9.
CC The invention relates to human B7-4 secreted (B7-4S) protein. B7-4
CC membrane (B7-4M) protein and their corresponding CDNA molecules. Human
CC B7-4 proteins are useful for upregulating immune response to treat viral
CC skin diseases such as Herpes disease or shingles disease, systemic viral
CC diseases such as influenza, common cold and encephalitis, and for
CC inducing tumour immunity or to downregulate an immune response useful in
CC organ transplants, graft-versus-host disease (GVHD), treating allergies
CC and viral infections e.g., acquired immune deficiency syndrome (AIDS).
CC B7-4 antagonists are used to modulate the T cell co-stimulation by
CC contacting an activated T cell with a B7-4 antigen. The invention is also
CC used for producing non-human transgenic animals. It also provides B7-4
CC fusion proteins which are useful for treating immunological disorders,
CC such as autoimmune diseases or in the case of transplantation. B7-4
CC fusion proteins are used as immunogens to produce anti-B7-4 antibodies.
CC B7-4 CDNA is also useful for gene mapping. Methods are provided
CC for modulating the immune response of individuals, by inhibiting or
CC enhancing the lymphokine synthesis by the activated T cells. Diagnostic,
CC prognostic, pharmacogenetics, screening and therapeutic methods are also
CC provided using B7-4 proteins.

50 Sequence 1553 BP; 467 A; 312 C; 384 G; 390 T; 0 other:

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Quality: 1511.00 Length: 290
Ratio: 5.210 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-649-108-1 x AAD02708

Align seg 1/1 to: AAD02708 from: 1 to: 1553

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17 nAlaPheThrValThrValProLysAspLeuTyrValAlaGluTyrGly 34
103 CGCATTTACTGTACGCTTCCAGAGACTATATGTGTAGAGTATGGTAA 152
34 eAsnMetThrIIeGluCysLysPheProValGluLysGlnLeuAspLeu 50
153 GCAATATGACATTCATGCAATTCGCCAGTAGAAACAAATAGACCTG 202
51 AlaAlaLeuIIeValTyrTrpGluMetGluAspLysAsnIIeIIeGln 67
203 GCTGCACCTAATTGCTATGTGGAATGAGAGATTAACAATATTCAAT 252
67 eValHisGluGluGluAspLeuLysValGlnHisSerSerTyrArgGln 84
253 TGTGATGAGAGAGAGAGACTGAAGGTTAGCATGACTACAGACACA 302
84 rGAlaArgLeuLeuLysAspGlnLeuSerLeuGlyAsnAlaAlaLeuGln 100
303 GGGCCGGCTGTGAAGGACAGCTCTCCCTGGAAATGCTGCACCTTCA 352
101 IIeThrAspValLysLeuGlnAspAlaGlyValTyrArgCysMetIIe 117
353 ATCAAGATGTAATAATTCAGAGATGACGGGTGTAACCTGCATGATCA 402
117 rTyrGluGlyAlaAspTyrLysArgIIeThrValLysValAsnAlaPro 134
403 CTATGGTGGTCCGACTACAGCGAATTACTGTGAAGCAATAGCCCCAT 452
134 yrAsnLysIIeAsnGlnArgIIeLeuValValAspProValThrSerGlu 150
453 ACAACAAATCAACCAAAATTTTCTGCTGTGATCCATCACCCTTGAA 502
151 HisGluLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIIe 167

503 CATGAACATGATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTG 512
167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrAsn 191
553 GACAACACTGACCATCAAGTCTGAGTGTAGACACACACCAACCAAT 602
184 eLysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIIeAsn 200
603 CCAGAGAGAGGAGAAAGCTTTTAATGTACCGACACACTGAGAAATCAG 652
201 ThrThrThrAsnGluIIePheTyrCysThrPheArgArgLeuAspPro 217
653 ACAACAACTAATGAGATTTCTACTGCACTTTAGAGATTACATCTGCA 702
217 uGluAsnHisThrAlaGluLeuValIIeProGluLeuProLeuAlaHis 234
703 GGAACACCATACAGCTGAATGGTCAATCCAGAACTACCTCTGCAATC 752
234 rProAsnGluArgThrHisLeuValIIeLeuGlyAlaIIeLeuLysCys 250
753 CTCCAATGAAAGACTCACTGTTATTTCTGGAGACCATCTATTATATG 802
251 LeuGlyValAlaLeuThrPheIIePheArgLeuArgLysGlyArgMet 267
803 CTGCTGTAGACACTGACATTCATCTCCGTTAAAGAAAGGAGAA1GAT 852
267 tAspValLysLysCysGlyIIeGlnAspThrAsnSerLysLysGlnSer 281
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903 ATACACATTTGGAGAGACG 922
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ID AAD05053 standard: cDNA; 3568 BP.
XX
AC AAD05053:
XX
DT 17-JUL-2001 (first entry)
XX
DE Human secreted protein-encoding gene 1 cDNA clone HDPAP35, SEQ ID NO:11.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; B7-H6 protein;
KW endocrine disorder; infection; wound healing; vulnerability; gene therapy;
KW cell culture; chemotaxis; food additive; chromosome 9;
KW binding partner identification; ss.
XX
OS Homo sapiens.
XX
XX
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XX FT sig_peptide 62..115
XX FT /*tag= b
XX FT mat_peptide 116..931
XX FT /*tag= c
XX FT /product= "Mature human secreted B7-H6 protein"
XX PN WO200134768-A2.
XX PD 17-MAY-2001.
XX

KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
KM AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW neurodegenerative disease; Parkinson's disease; ss.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
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FT /product= "TANGO 509"
FT /note= "The coding sequence (ORF) is specifically
FT sig_peptide 59..112 claimed in Claim 1"
FT /tag= b
FT mat_peptide 113..929
FT /tag= c
XX
XX WO200121631-A2.
XX
XX P 29-MAR-2001.
XX
XX PF 20-SEP-2000; 2000WO-US25982.
XX
XX PR 20-SEP-1999; 99US-0399723.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;
XX
XX DR WPI: 2001-211461/21.
XX P-PSDB: AAU01362.
XX
XX PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
XX 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
XX PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
XX disease -
XX
XX PS Claim 1; Fig 22; 362pp; English.
XX
XX CC The sequence represents the coding sequence of human TANGO 509
XX CC transmembrane protein. The nucleic acid and polypeptide sequences
XX CC are useful for the diagnosis, prognosis and treatment of immunological
XX CC disorders (e.g. arthritis, graft rejection and acquired immunodeficiency
XX CC syndrome), inflammatory disorders (e.g. psoriasis and asthma), renal
XX CC disorders, embryonic disorders, brain-related disorders (e.g. cerebral
XX CC oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-
XX CC related disorders, pituitary-related disorders (e.g. Cushing's disease)
XX CC and neurodegenerative diseases (e.g. Parkinson's disease).
XX
XX Sequence 3575 BP; 1029 A; 717 C; 738 G; 1091 T; 0 other;

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Quality: 1511.00 Length: 290
Ratio: 5.210 Caps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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17 nalalphenrvalthrvalprolysaspheutyrvalvalglutyrglys 34
|||||
109 CGCATTTACTGTCAGGTTCCCAAGACCTATATGTGTGAGAGTATGGA 158
34 erAsmethrilleglucylsypheprovalglulysglinleuaspleu 50
|||||

159 GCATATGCAATTTGAATGCATTAATCCAGTAGAAAAACATATAGACTTG 208
51 Alalalaleuilevallyrrtpglumetgluasplyasnllelleghlph 67
|||||
209 GCTGCACATAATGCTCTATTGGGAAATGAGAGATMAAACATATATCAAT 258
67 evalhlsiglygluaspleuysvalglinhlsesertertyrarglna 84
|||||
259 TGTGCATGGAGAGAGAGACCTGAGGTTCCAGCATAGTACTACACACAGA 308
84 rgalalargleuleuysaspgluleuSerleuylasnalalaleuileu 100
309 GGGCCCGCGCTGTTGAAGGAGACCACTCTCCCTGGGAATGCTGCACITCA 358
101 llethrAspyallysleuGlinalaglyvaltyrArgysmethlles 117
|||||
359 ATCACAGATGTGAAATTTGAGGATGACGGGCTGTACCGCTGCATGATCA 408
117 rtyrlygllyalaaspyrrlysrargllethrvallysvalasnalal 111
409 CTATGCTGCTGCCGACTACAGCGCAATTTACTGTGAAGTCATATGCCCAT 458
134 yrasnlyslleasnGlinalarglleuvalvalasprovalthrserglu 150
459 ACACAAATCAACCAAGAAATTTGTTGTGTGATCCAGTCACCTCTGAA 508
151 hisgluleuthrcysglinalaglytyrprolysalaGluallethr 167
|||||
509 CATGAACATCAATGTCAGGCTGAGGCTACCCCAAGCCGCAACATCATCT 558
167 pthrserAspHisglinValleuSerlylsthrrthrThrAsn 184
559 GACACACAGTACCATCAAGTCTGAGTGTAGACACACACACCAACAT 608
184 eflysarglglululsleupheasnvalthrserthrleuargleasn 200
609 CCNAGAGAGAGAGAGAGCTTTCAATGTGACACGACACTGAGATACAC 658
201 thrrthrThrAsnGlulilephtyrCysthrPheargArgleuasprcgl 217
659 ACACACACTAATGAGATTTTCTACTGCTACTTTAGAGATTAATGATCTGA 708
217 ugluaSnHsthrAlaGluleuvalilleprogluleuProleuAlaHsp 234
709 GGAACACATACAGCTGATTTGCTATCCACAGACACTGCTGACATC 758
234 robProasnGlualrghrHlsleuvalilleuGllyalilleuLeu 250
759 CTCCAATGAAGAGACTCTTGTAATCTGGAGCCCATCTTAATATGC 808
251 leuGlyValAlaleuthrPhelePheargleuArglysllyrrqmetwe 267
809 CTTCGTGTAGCACTGACATTCATCTTCGTTAAGAAAGGAGAAATGAT 854
267 laspyallyslyscysgllylleGlnasprthrasnseryllyslsery 284
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284 spThrHlsleuGluluthr 290
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ID AAS06592 standard; cDNA: 3616 BP.
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AC
XX
XX 26-SEP-2001 (first entry)
DT
XX
XX Human immunoregulatory protein B7-H1 cDNA sequence.
DE
XX

KW Human: immunoregulatory protein; B7-H1; co-stimulating T-cell;
KW B-cell antibody-producing response; IgG2a antibody response; APC;
KW Immunodeficiency disease; inflammatory disease; autoimmune disease;
KW antigen presenting cell; pathologic cell mediated disease; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 73..945
FT /*tag- a
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FT sig_peptide 73..138
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FT maL-peptide 139..942
FT /*tag- c
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XX WO200139722-A2.
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XX 07-JUN-2001.
XX
XX P 30-NOV-2000; 2000MO-US32583.
XX
XX PR 30-NOV-1999; 99US-0451291.
XX PR 28-AUG-2000; 2000US-0649108.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX PI Chen L;
XX
XX WPI: 2001-397926/42.
XX
XX DR P-PSDB; AAU03559.
XX
XX PT Novel DNA encoding immunoregulatory molecule B7-H1, is useful for
XX PT co-stimulating a T cell for augmenting immunoregulation and for
XX PT controlling pathologic cell mediated conditions -
XX
XX PS Example 2: Fig 1; 85pp; English.
XX
XX CC The present sequence encoding for novel human immunoregulatory protein
XX CC B7-H1 (B7-H1) is capable of co-stimulating T-cells. The sequence for
XX CC mouse B7-H1 (mB7-H1) is also given (AAU03560). B7-H1 is useful for
XX CC co-stimulating T-cells such as helper T-cells that provide helper
XX CC activity for B-cell antibody-producing response e.g. IgG2a antibody
XX CC response, in a mammal having an immunodeficiency disease, inflammatory
XX CC condition or an autoimmune disease, by culturing B7-H1 with the
XX CC mammalian T-cells in vitro, or administering B7-H1 or a nucleic acid
XX CC encoding B7-H1 to the T-cells, such that the level of CD40 ligand on the
XX CC T-cell surface is increased. The method further involves providing a
XX CC recombinant cell e.g. an antigen presenting cell (APC) which is the
XX CC progeny of a cell obtained from the mammal and has been transfected or
XX CC transformed ex vivo with a nucleic acid encoding B7-H1, so that the cell
XX CC expresses B7-H1, and administering the cell to the mammal. Prior to
XX CC administration, the APC is pulsed with an antigen or an antigenic
XX CC peptide. B7-H1 can be used to control pathologic cell mediated
XX CC conditions (e.g. those induced by infectious agents such as Mycobacterium
XX CC tuberculosis) or other pathologic cell mediated responses such as those
XX CC involved in autoimmune diseases (e.g. rheumatoid arthritis).
XX
XX SQ Sequence 3616 BP; 1059 A; 726 C; 739 G; 1092 T; 0 other;

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Quality: 1511.00 Length: 290
Ratio: 5.210 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 nalalphehrvalthrvalprolysaspleutyvalvalglutryglys 34
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123 CGCATTTACTGACAGGTTCCAGAGACCTATATGGTAGATGTA 172
34 erAsmetthrleglucyslyspheprovalglulysgluleuaspheu 50
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173 GCAATATGACAAATTCGAATGCCAGTGAAGAAACAAATTCAGCTG 222
51 Alaalaleullelvaltyrrpplumetlunsplysaenillelglph 67
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223 GCTGCATTAATTGCTATTGGAAATGAGATTAAGCAATTATTCATTT 272
67 evalhlslyglugluaspheulysvalgluhlsersertrfayrglna 84
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273 TGTGCATGAGAGAGAGACCTGAAGGTTCCAGCATAGTACACACAGA 322
84 rgalaargleuleulelysaspclnleuserleuglyasnalaaleucln 1004
323 GGGCCGGCTGTGAAAGACCGCTCTCCGGAATGCTGCATTCAG 372
101 llethraspevallysleuglnaspalacllyvaltyrargysmetlise 117
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373 ATCACAGATGTGAATTCAGAGATCAGGGGTATCCCTCATGATCATCAG 422
117 rTyrglylvalalaspTyrrlysargllethrvalylsvalasnalaproV 1344
|||||||||||||||||||||||||||||||||||||||||||
423 CTATGGTGTGGCCGACTCAAGCGAATTACTGTGAAGCATATGCCCAT 472
134 yfAsnlyslleasnlnarglyleuvalvalaspProvalthrserrln 150
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473 ACNACMAAATCAACCAAGAAATTTGGTGGAGTCAACCTCACTGAA 522
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523 CATGAACTGACATGTCAGGCTGAGGCTACCCCAAGGCCGAAGTATCTG 572
167 pThrsersAsphlslnvalleuserglylysrthrrthrrasns 184
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573 GACACAGAGTGCATCAAGTCTCAGTGTAAAGACCAACCAACCATTT 622
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|||||||||||||||||||||||||||||||||||||||||||
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201 ThrtrrrrasngluillephetyrcysThrpheargafgleuaspProgl 217
673 ACAACAACTAATGACATTTTCTACTGCACTTTTAGGAGATTAGATCTGA 722
217 uGluasnhrsthralaglualeuvalilleprogluleuProleuAlahsp 234
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723 GGAAACCATTCAGCTGATGATGGTCATCCAGAACTACCTCTGGCACATC 7724
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251 leuglyValalaleuthrPhelIepheargleuarglysglyarCmetme 267
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823 CTGGGTAGACACTGACATTCATCTCCGTTTAAAGAAAAGGAGATATAT 872
267 tAspValylslyscysglyllelnAspThrAsnserlyslsnglnsra 284
873 GGATGTGAATAAATGTGGCATTCGAAGATNACAACCAAGCAAGCAACTG 9224
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seq_name: /STDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.AAS02118
seq_documentation_block:

ID AAS02118 standard; cDNA: 3575 BP.
XX
AC AAS02118:
XX
DT 18-JUL-2001 (first entry)
XX
DE Human TANGO 509, alternative cDNA sequence #1.
XX
KW Human: TANGO 499; transmembrane protein; diagnostic; asthma;
KW Immunological disorder; arthritis; graft rejection; renal disorder;
KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
KW neurodegenerative disease; Parkinson's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..931
FT /*tag= a
FT /product= "TANGO 509, alternative transmembrane
protein #1"
XX
XX MO200121631-A2.
XX
XX 29-MAR-2001.
XX
XX 20-SEP-2000; 2000MO-US25982.
XX
XX 20-SEP-1999; 99US-0399723.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;
XX
XX DR WPI: 2001-211461/21.
XX
XX P-PSDB: AAU01407.
XX
XX PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
PT 351, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
PT disease.
XX
XX PS Disclosure: Page 342-344; 362pp; English.
XX
XX CC The sequence represents the coding sequence of human TANGO 509,
CC alternative transmembrane protein #1. The nucleic acid
CC and polypeptide sequences are useful for the diagnosis, prognosis and
CC treatment of immunological disorders (e.g. arthritis, graft rejection and
CC acquired immunodeficiency syndrome), inflammatory disorders (e.g.
CC psoriasis and asthma), renal disorders, embryonic disorders, brain-
CC related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g.
CC ischaemia), tumours, prostate-related disorders, pituitary-related
CC disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g.
CC Parkinson's disease).
XX
XX SQ Sequence 3575 BP; 1030 A; 717 C; 738 G; 1090 T; 0 other;

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Quality: 1508.00 Length: 290
Ratio: 5.200 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.655

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US-09-649-108-1 x AAS02118
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59 ATGAGGATATATGCTGCTTTTATATTCATGACCTACTGCAATTTGCTGAA 108

17 nAlaPheThrValThrValProLysAspLeuTyrValValGluTyrGlyS 34
|||||
109 CGCATTTACTGTCACGGTTCCAAAGACCTATATGCTAGAGTATG3TA 1*
34 eRasnMetThrIleGluCysLysPheProValGluLysGlnLeuAspLeu 50
|||||
159 GCAATATGACAAATTGAATGCAAAATTCGCCATAGAAAAACATATTAACCTC 208
51 AlaIleuIleValIleTyrTrpGluMetGluAspLysAsnIleIleGlnP 67
|||||
209 GCGCACTAATTCCTATTCGGAAATGAGATGAGATAGAACATTTATTCANT 258
67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTyrArgGlnA 84
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259 TGTGCATGGAGAGAGACCTGAAGGTTCCAGCATAGAGCTACACACACCA 108
84 rGAlaArgLeuLeuLysAspGlnLeuSerLeuGlnAsnAlaIleLeuGln 100
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101 IleThrAspValLysLeuGlnAspAlaGlyValIleTyrArgCysMetIle 117
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359 ATCACAGATGTGAATTCGAGATGACAGGGGTGTACCGCTGCATGACATCAG 408
117 rTyrGlyGlyAlaAspTyrLysArgIleThrValLysValAsnAlaProT 134
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134 yRAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGln 150
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459 ACAACAAATCAACCAAGAAATTTGGTGTGATCCAGTCACCTCTCGAA 508
151 HisGluLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIleT 167
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509 CATGAACCTGACATGTCAGGCTGAGGGCTACCCCAAGGCCGCAAGTCATCTG 558
167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrThrAsnS 184
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559 GACACACATGACCATCAAGTCTGAGTGTAGACACACCAACCAAT 608
184 eRysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
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609 CCAAGAGAGAGAGAGAGCTTTTCAATGTGCACGACACATGAGAAATCAAC 658
201 ThrThrThrAsnGluIlePheTyrCysThrPheArgArgLeuAspProG 217
|||||
659 ACAACACTAATGAGATTTTCTACTGCACCTTTTAGGATTAGATCTCTGT 708
217 uGluAsnHisThrAlaGluLeuValIleProGluLeuProLeuAlaHisP 234
|||||
709 GGAACACATACACGCTGAATGGTTCATCCGAACTACCTCTGGCACATC 758
234 rProAsnGluArgThrHisLeuValIleLeuGlyAlaIleLeuLeuCys 250
|||||
759 CTCCAATGAAGAGACTCTGTGTAATCTGGAGGACCATTTATTAATG 808
251 LeuGlyValAlaLeuThrPheIlePheArgLeuArgLysGlyArgPheMet 267
|||||
809 CTTGGTGTAGCACTGACATTCATCTCCGTTTAAGAAAAGGGAATGAT 858
267 rAspValLysLysCysGlyIleGlnAspThrAsnSerLysGlyGlnSerA 284
|||||
859 GGAATGAAAAAATGTGGCATCCCAAGATCAAACTCAAAAGACCAAAAGTG 908
284 sPThrHisLeuGluGluThr 290
|||||
909 ATACACATTTGGAGAGACG 928

seq_name: /SID2/gcgcdata/geneseq/geneseqn/MA2001.DAT:AAS02120
seq_documentation_block:
ID AAS02120 standard; cDNA: 3575 BP.
XX


```

18-JUL-2001 (first entry)
XX DE Human TANGO 509, variant cDNA sequence #4.
XX KW Human; TANGO 499; transmembrane protein; diagnostic; asthma;
XX KW immunological disorder; arthritis; graft rejection; renal disorder;
XX KW acquired immunodeficiency syndrome; inflammatory disorders; psoriasis;
XX KW AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour;
XX KW prostate; cerebrovascular disease; pituitary; Cushing's disease;
XX KW neurodegenerative disease; Parkinson's disease; ss.
XX OS Homo sapiens.
XX FH
XX FT Key Location/Qualifiers
XX FT CDS 59..931
XX FT /*tag= a
XX FT /product= "TANGO 509, variant transmembrane
XX FT protein #4"
XX PR WO200121631-A2.
XX PR 29-MAR-2001.
XX PE 20-SEP-2000; 2000WO-US25982.
XX PR 20-SEP-1999; 99US-0399723.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Kirst SJ, Sharp JD, Fraser CC, Barnes T, Kingsbury G;
XX PI WPI: 2001-211461/21.
XX DR P-PSDB; AA001410.
XX PT New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO
XX PT 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
XX PT for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
XX PT disease -
XX PS Disclosure; Page 352-354; 362pp; English.
XX CC The sequence represents the coding sequence of human TANGO 509,
XX CC variant transmembrane protein #4. The nucleic acid and polypeptide
XX CC sequences are useful for the diagnosis, prognosis and treatment of
XX CC immunological disorders (e.g. arthritis, graft rejection and acquired
XX CC immunodeficiency syndrome), inflammatory disorders (e.g. psoriasis and
XX CC asthma), renal disorders, embryonic disorders, brain-related disorders
XX CC (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemia),
XX CC tumours, prostate-related disorders, pituitary-related disorders (e.g.
XX CC Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's
XX CC disease).
XX XX
XX Sequence 3575 BP; 1029 A; 718 C; 737 G; 1091 T; 0 other;
XX
alignment_scores:
Quality: 1508.00 Length: 290
Ratio: 5.200 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.655
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1 McLaArgIlePheAlaValPheIlePheMetThrTyrTrpHisIleuLeuAs 17
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59 ATGAGCATATTGGCTGCTCTTAATATCATGACCTACTGCGATTGGCTGAA 108
|||||
17 nAlaPheThrValThValProlAspIeuTyrValValAlaGluTyrGlyS 34
|||||
109 CGATTACTGTCACGGTCCCAAGGACCTATATGTGGTAGAGATATGGTA 158
|||||

```

34 eTasmeTethrIleGluGlySerPheProValIGluGlyGlnLeuAspLeu 50
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159 GCAATATGACAAATTGAAATGCAAAATTTCCAGATCAAAAAAATTAAGACTTG 208
51 ALaAlaLeuIleValTYrTgJlWetGluAspLysAsnIleIleGlnPh 57
|||||
209 GGTGCACATAATTGCTATTGGGAAATGGAGGATAGAAGAACTAATTCATT 258
67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTYrArgLna 84
|||||
259 TGTGATGAGAGGAGGAAGACTGAAGGTTGACACATAGACATGACAGACA 308
84 rGAlaArgLeuLeuLysAspGlnLeuSerLeuGlnAsnAlaIleAsn 100
GGGCCCCGGCTGTGAGGAGCAGACTCTCCCTGGGAAATGCTGCACCTTCAG 309
101 lIeThrAspValLysLeuGlnAspAlaGlyValTYrArgCysMetIleSe 117
ATCACAGATGTGAATTTGCAGATGCAGGGGTGATACGGCTCATGATCAG 359
117 rTYrGlyGlyAlaAspTYrLysArgIleThrValLysValAsnAlaProT 134
|||||
409 CTAATGCTGCTGCCGACTCAAGCCGAATTAACGTAAATCATATCCCAT 458
134 yTAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGlu 150
ACACAAATATCACCAAGAAATTTGGTGTGGATCCAGTCACTCTCGTGA 459
151 HisGluLeuThrCysGlnAlaGluGlyTYrProLysAlaGluValIleTr 167
CATGAACATGACATCTCAGCTGAGGGCTACCCCAAGGCCGAGATCACTG 509
167 pHisSerSerAspHisGlnValLeuSerGlyLysThrThrThrTrpAsn 184
|||||
559 GCAAGCCATGACATCAAGTCTGAGTGTGAAGACCAACCAACCAAT 608
184 ePLeuArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
|||||
609 CCAAGAGAGAGAGAAGCTTTTCATGTCAGCACACACTGAGANTCAAC 658
201 ThrThrThrAsnGluIlePheTYrCysThrPheArgArgLeuAspProGlu 217
|||||
659 ACAACAACATAAGAAATTTTCTACTGCACCTTTAGGAGATTAAGATCTGA 709
217 uGluAsnHisThrAlaGluLeuValIleProGluLeuProLeuAlaHisP 234
GGAAAAACCATACAGCTGAATTGGTGCATCCGAACACTACCTCTGGCACATC 758
234 rOProAsnGluArgThrHisLeuValIleLeuGlyAlaIleLeuLeuCys 255
CTCCAAATGCAAAAGGACTCACTGTGTAATTCGGGAGGCCATCTTATTATGC 759
251 LeuGlyValAlaLeuThrPheIlePheArgLeuArgLysGlyArgMetIle 267
CTTGGTGTGAGCCTACATCTCTCTCCGTTTAAGAAAAAGGAGAAATGAT 809
809 CTTGGTGTGAGCCTACATCTCTCTCCGTTTAAGAAAAAGGAGAAATGAT 858
267 rAspValLysLysCysGlyIleGlnAspThrAsnSerLysLysGlnSerVal 284
|||||
859 GGATGTGAAAAAATATGTGGCATTCAGAGATACAAACTCAAGAAAGCAAGTG 908
284 sPTHisIleGlnGluLuhTr 290
|||||
909 ATACACATTGGAGGAGACG 928
seq_name: /SIDS2/gcdata/geneseq/geneseqn/NA2001.DAT:AS02119,
seq_documentation_block:
ID AS02119 standard; cDNA; 3575 BP.
XX AS02119;
XX
XX 18-JUL-2001 (first entry)

Human; B7-4 secreted protein; B7-4S; receptor PD-1; chromosome 9; tumour; antiviral; antiasthmatic; gene mapping; cytostatic; myocardial infarction; atherosclerosis; neurological disease; immunomodulatory; allergy; GVHD; graft-versus-host disease; immunosuppressive disease; organ transplant; acquired immune deficiency syndrome; AIDS; autoimmune disease; therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 59..796

FT /tag= a

FT /product= "Human B7-4 secreted (B7-4S) protein"

FT sig_peptide 59..112

FT /tag= b

FT mat_peptide 113..793

FT /tag= c

FT /product= "Mature human B7-4 secreted (B7-4S) protein"

FT /note= "Serves as an extracellular domain"

XX MO200114557-A1.

XX PD 01-MAR-2001.

XX 23-AUG-2000; 2000MO-US23347.

XX 23-AUG-1999; 99US-0150390.

XX 10-NOV-1999; 99US-0164897.

XX (DAND) DANA FARBER CANCER INST INC.

XX (GENY) GENETICS INST INC.

XX Wood C, Freeman GJ;

XX WPI: 2001-160116/16.

XX P-PSDB: AAY72676.

XX Treating e.g. cancer or allergies comprises contacting an immune cell with an agent that modulates signaling via PD-1 or B7-4 to modulate the immune response -

XX Example 1; Fig 1; 168pp; English.

XX The present CDNA sequence encodes human B7-4 secreted (B7-4S) protein having a short hydrophilic tail without a membrane anchor or a transmembrane domain. The human B7-4 CDNA is isolated from human activated keratinocyte and placental cDNA libraries. B7-4 gene is localized on human chromosome 9.

XX The invention relates to a method for modulating immune response by contacting an immune cell with an agent that modulates signaling via B7-4 or its receptor PD-1. Modulating the interaction between PD-1 and B7-4 modulates a costimulatory or an inhibitory signal in an immune cell, resulting in the modulation of the immune response. The invention is useful for upregulating an immune response to treat tumours, neurological diseases and immunosuppressive diseases or to downregulate an immune response useful in organ transplants, graft-versus-host disease (GVHD), treating allergies and viral infections e.g., acquired immune deficiency syndrome (AIDS). The invention also provides B7-4 or PD-1 fusion proteins which are useful for treating immunological disorders, such as autoimmune diseases e.g., heart disease, myocardial infarction and atherosclerosis or in the case of inhibiting rejection of transplants. These fusion proteins are also used as immunogens to produce anti-B7-4 antibodies.

XX PD-1 is useful in promoting the maintenance of pregnancy. B7-4 protein is highly expressed in placental trophoblasts and plays a role in preventing maternal rejection of the foetus. B7-4 CDNA is also useful for gene mapping.

XX Sequence 968 BP; 314 A; 209 C; 202 G; 243 T; 0 other;

alignment_scores:

Quality: 1184.00

Ratio: 5.216

Length: 227

Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-649-108-1 x AAD02772 ..

Align seg 1/1 to: AAD02772 from: 1 to: 968

1 MetArgIlePheAlaValPheIlePheMetThrTyrTrpHisLeuAsn 17

59 ATGAGATATTGCTGCTTATATTCATGACCTACGCGCATTTGCTGAA 108

17 nAlaPheThrValThrValProLysAspLeuTyrValValGluTyrGly 34

109 CGCATTTACTGTCACGGTTCCCAAGACCTATATGTGTGATGAGTATG 158

34 eAsnMetThrIleGluCysLysPheProValGluLysGlnLeuAspLeu 50

159 GCAATATGACAAATTGAATGCCAATTCCTCCATGAAAAACAATTAGAC 208

51 AlaAlaLeuIleValTyrTrpGluMetGluAspLysAsnIleIleGlnP 67

209 GCTGCACCTAATTTGCTTATTTGGGAAATGAGGATPAGAACATTAACA 258

67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTyrArgGln 84

259 TGTGCATGGAGAGAGAGACCTGAAGGTTCCAGCATAGTACAGACAGA 308

84 rGlaIaArgLeuLeuLysAspGlnLeuSerLeuGlnAsnAlaIaLeuGln 100

309 GGGCCCGCGCTGTGAAGGACACCTCTCCCTGGGAAATGCTGCACAT 358

101 IleThrAspValLysLeuGlnAspAlaGlyValTyrArgGlyMetIle 1

359 ATCAGAGATGTGAATTCGACGATGACAGGGGTGTACCGCTGCATGATC 408

117 rTyrGlyGlyAlaAspTyrLysArgIleThrValLysValAsnAlaPro 114

409 CTATGGTGGCGCCGACTACAGCGAATTACTGTGAAGTCAATGCCCAT 458

134 yAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGln 1

459 ACAACAATAATCAACCAAGAATTTGGTGTGATCCAGTCACCTCTGAA 508

151 HisGluLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIle 167

509 CATGACCTGACATGTCAGGCTGAGGCTTACCCCAAGGCCGAACTCAT 558

167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrAsn 184

559 GACAAGCAGTACCATCACTCACTGAGTGTAGACCAACCAACCACTAT 608

184 eLysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200

609 CCAAGAGAGAGAGAAAGCTTTTCAATGTGACACAGACATGAAATCA 658

201 ThrThrThrAsnGluIlePheTyrCysThrPheArgArgLeuAspPro 217

659 ACAACAACCTAATGAGATTTTCTACTGCACCTTTAGGAGATTAATCT 708

217 uGluAsnHisThrAlaGluLeuValIlePro 227

709 GGAACAACATACAGCTGAATTTGTCATCCCA 739

seq_name: /SID52/gcgsdata/geneseq/geneseqn/NA2001.DAT:AAE02772

seq_documentation_block:

ID AAD02707 standard; CDNA; 968 BP.

AC AAD02707;

XX 31-MAY-2001 (first entry)

DT XX Human B7-4 secreted (B7-4S) protein cDNA.

DE

```

XX Human: B7-4 secreted protein; B7-4S; chromosome 9; antiviral; influenza;
KM immunomodulatory; acquired immune deficiency syndrome; AIDS; anti-tumour;
KM graft-versus-host disease; GVHD; immunological disorder; Herpes disease;
KM autoimmune disease; common cold; shingles disease; encephalitis; therapy;
KM organ transplant; gene mapping; transgenic; viral infection; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..796
FT /tag= a
FT /product= "Human B7-4 secreted (B7-4S) protein"
FT sig_peptide 59..112
FT /tag= b
FT mat_peptide 113..793
FT /tag= c
FT /product= "Mature human B7-4 secreted (B7-4S) protein"
FT /note= "Serves as an extracellular domain"
XX
P NO200114556-A1.
XX
PD 01-MAR-2001.
XX
PF 23-AUG-2000; 2000MO-US23256.
XX
PR 23-AUG-1999; 99US-0150390.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Freeman G, Bousiotis V, Chernova T, Malenkovich N;
XX
DR WPI: 2001-202936/20.
DR P-SDB: AAY72644.
XX
PT New human B7-4 polypeptides useful for enhancing the immune response
PT against a viral infection or induce a tumor immunity and to diagnose
PT conditions related to aberrant B7-4 expression or activity
XX
PS Claim 1: Fig 1: 123pp: English.
XX
XX The present cDNA sequence encodes human B7-4 secreted (B7-4S) protein
CC having a short hydrophilic tail without a membrane anchor or a
CC transmembrane domain. Human B7-4 protein is isolated from human activated
CC keratinocyte and placental cDNA libraries. B7-4 gene is localised on
CC human chromosome 9.
CC The invention relates to human B7-4 secreted (B7-4S) protein, B7-4
CC membrane (B7-4M) protein and their corresponding cDNA molecules. Human
CC B7-4 proteins are useful for upregulating immune response to treat viral
CC skin diseases such as Herpes disease or shingles disease, systemic viral
CC diseases such as Influenza, common cold and encephalitis, and for
CC inducing tumour immunity or to downregulate an immune response useful in
CC organ transplants, graft-versus-host disease (GVHD), treating allergies
CC and viral infections e.g., acquired immune deficiency syndrome (AIDS).
CC B7-4 antagonists are used to modulate the T cell co-stimulation by
CC contacting an activated T cell with a B7-4 antigen. The invention is also
CC used for producing non-human transgenic animals. It also provides B7-4
CC fusion proteins which are useful for treating immunological disorders,
CC such as autoimmune diseases or in the case of transplantation. B7-4
CC fusion proteins are used as immunogens to produce anti-B7-4 antibodies.
CC B7-4 cDNA is also useful for gene mapping. Methods are provided
CC for modulating the immune response of individuals, by inhibiting or
CC enhancing the lymphokine synthesis by the activated T cells. Diagnostic,
CC prognostic, pharmacogenetics, screening and therapeutic methods are also
CC provided using B7-4 proteins.
XX
SQ Sequence 968 BP; 314 A; 209 C; 202 G; 243 T; 0 other:

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alignment_scores:
    Quality: 1184.00      Length: 227
    Ratio: 5.216          Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

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US-09-649-108-1 x AAD02707
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59 ATGAGCATATTTGCTGCTCTTATATTCATGACCTACCTGCACTTCTGCA 108
17 nAlaPheThrValThrValProLysAspLeuTyrValValLeuTyrGlyS 17
109 CGCATTTACTGTCCACGGTTCCCAAGGACCTATATGTTGGTACAGATGCTA 158
34 eAsnMetThrTleGluCysLysPheProValGluLysGlnLeuAspLeu 50
159 GCATATATGACAAATTGAATGCAAAATTTCCAGTAGAAGAAACAAATTAGACCTG 208
51 AlaAlaLeuIleValTyrTrpGluMetGluAspLysAsnIleIleGlnP 67
209 GCTGCACATAATTGCTTATTGGGAATGGAGGATTAAGAACATTATTCATTT 258
67 eValHisGlyGluGluAspLeuLysValGlnHisSerSerTyrArgGln 84
259 TGTGCATGTAGAGAGAAAGACTGAAAGTTCCACATATAGTACGACACAGA 304
84 rGAlaArgLeuLeuLysAspGlnLeuSerLeuGlyAsnAlaLeuGln 100
309 GGGCCCGGCTGTGAAAGAGCCAGCTCTCCCTGGGAATGCTGCACCTTCAG 358
101 IleThrAspValLysLeuGlnAspAlaGlyValTyrArgCysMetIleSe 117
359 ATCACAGATGTGAATTCAGAGATCCAGGGGTGACCCCTCATGATCAG 408
117 rTyrGlyGlyAlaAspTyrLysArgIleThrValLysValAsnAlaProT 134
409 CTATGGTGTGGCCGACTACAAAGCGAATTAAGTGAATCATATGCCCCAT 458
134 yAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGlu 150
459 ACAACAAATTCACCAAGAAATTTGGTTGGATCCAGTCACCTCTTCGAA 508
151 HisGluLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIleTr 167
509 CATGACATGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTG 524
167 pThrSerSerAspHisGlnValIleuSerGlyLysThrThrThrTrpAsn 184
559 GACAAGCAGTACCATCAAGTCCTGAGTGTAAAGCCACACACACCATTT 608
184 eLysArgGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
609 CCAACAGAGAGAGAGAAAGCTTTTCATGTCAGACACACACATGAAATCAG 658
201 ThrTrpThrAsnGluIlePheTyrCysThrPheArgValGluAspProG 217
659 ACAACAACTAATAGAGATTTTCTACTGCACTTTAGACAGATTAGATTCCTCA 708
217 uGluAsnHisThrAlaGluLeuValIlePro 227
709 GGAAACCATATACAGCTGAATTGGTCAATCCCA 739

seq_name: /SID52/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH14847
seq_documentation_block:
ID AAH14847 standard; cDNA; 1301 BP.
XX
AC AAH14847:
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:12675.
XX

```

```
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PM EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
PM WPI: 2001-318749/34.
XX
PT primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 12675; 2537bp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 1301 BP; 387 A; 261 C; 327 G; 326 T; 0 other:
XX

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      Quality: 1181.00      Length: 228
      Ratio: 5.180      Gaps: 0
      Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
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79 rSerTYrArgGlnArgAlaArgLeuLysAspGlnLeuSerLeuGlyA 96
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52 TAGCTACAGACAGAGGCCGCTGTTGAAGGACGAGCTCTCCCTGGAA 101
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96 snAla1aLeuGln1leThrAspValLysLeuGlnAspAlaGlyValTyr 112
|||||
102 ATGCTGCACCTTCAGATCAGATCAGATGTAATTCAGATGAGGGGATG 151
|||||
113 ArgCysMetL1leSerTYrGlyAlaAspTYrLysArg1leThrValLy 129
|||||
152 CGCTGCATGATCAGTATGTTGGTGGCGACTACAGGAATTCGTGSA 201
|||||
129 sValAsnAlaProTYrAsnLysL1leAsnGlnArg1leLeuValAsp 146
|||||
202 ACTCAATGCCCCATACACAAATAACCAAGAAATTTGTTGTGATC 251
|||||
146 rovalThrSerGluH1sg1uLeuThrCysGln1laG1uGlyrProLys 142
|||||
252 CACTCACCTTGAAACATGAACATGATGCTGAGGGGCTACCCCAAG 301
|||||
163 Alag1uVal1leThrPThrSerAspH1sg1uValLeuSerGlyLysT 179
|||||
302 GCCGAAGTCATCTGAGCAAGCAGTGAACCATCAAGTCTGAGTGAAG 351
|||||
179 rThrThrThrAsnSerLysArgGluLysLeuPheAsnValThrSerT 346
|||||
352 CACCACCACCAATTCAGAGAGAGAGAGAGCTTTCATGATGACCA 401
|||||
196 hrLeuArg1leAsnThrThrThrAsnGlu1lePheTYrCysThrP 212
|||||
402 CACTGAGAAATCAACACACACAACTAATGAGATTTTCTACTGCTT 451
|||||
213 ArgLeuAspProGluGluAsnH1sThrAlaGluLeuVal1leProG 229
|||||
452 AGATTGATCTCGTAGGAAACCAATGAGTGAATTTGGTATCCAGACT 501
|||||
229 uProLeuAlaH1sProProAsnGluArgThrH1sLeuVal1leLeu 246
|||||
502 ACCTCGGCACATCTCCAAATGAAAGACTCACTTGTAATTCGTGG 551
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246 1a1leLeuLeuCysLeuGlyValAlaLeuThrPhe1lePheArgL 262
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552 CCATCTTATATGCTTGGTGTAGCACTGACATTCATCTCCGTTTAA 601
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263 LysG1YArgMetLaspValLysLysCysGly1leGlnAspThrAsn 279
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602 AAGGGAGATGATGATGATGTAATAAATGCGCATCCAAATCAAACT 651
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279 rLysLysGlnSerAspThrH1sLeuGluThr 290
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seq_name: /SIDS2/gcgsdata/geneseq/geneseqn/NA2001.DAT:AAH07571
seq_documentation_block:
ID AAH07571 standard; cDNA; 784 BP.
XX
AC AAH07571;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:4406.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PM EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
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XX W0200134768-A2.
XX
XX
PD 17-MAY-2001.
XX
XX 01-NOV-2000; 2000OWO-US30039.
XX
XX 09-NOV-1999; 99US-0164344.
PR 07-APR-2000; 2000OUS-0195296.
PR 27-JUL-2000; 2000OUS-0221367.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen HS, Komatsoulis G, Duan DR, Ebner R, Ruben SM;
XX WPI: 2001-308780/32.
DR P-PSDB: AAE01179.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 1: Page 410; 474pp; English.
XX
CC AAD05053-AAD05106 represent cDNAs corresponding to 15 human secreted
CC protein genes, and AAE01164-AAE01217 represent the proteins they encode.
CC AAE01218-AAE01226 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 15 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, hematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays (e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA)). The present sequence represents a human
CC secreted B7-H6 protein-encoding cDNA of the invention.
XX
XX Sequence 891 BP; 266 A; 203 C; 206 G; 215 T; 1 other;
SQ

alignment_scores:
Quality: 1177.00 Length: 227
Ratio: 5.208 Gaps: 0
Percent Similarity: 99.559 Percent Identity: 99.559

alignment_block:
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17 nAlaPheThrValThrValProLysAspLeuTyrValValGluTyrGlyS 34
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143 CGCATTTACTGTCACGTTCCCAAGACCTATATGTGTAGACTATGCTA 192

34 eraInMetThrIleGluCysLysPheProValGluIleuSgInleuAAspLeu 50
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193 GCATATATGACCAATTGAATGCAAAATTCCTCCAGTACAAAAACATTAAGACTG 242
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293 TCTGCATGAGAGAGAACCTGCAAGCTTCAGCATAGCTACAGACACAGA 342
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84 rglAlaArgLeuLeuLysAspGlnLeuSerLeuGlnsAlaIleuGlnIn 130
343 GGGCCCGCGCTGTGAAGACACCTCTCCCTGGGAATGCTGCATTCAG 392
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101 IleThrAspValLysLeuGlnAspAlaGlyValTyrArgCysMetIleSe 117
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443 CTATGCTGTGCGCGACTACAAAGCAATTTACTGTGAAGTCAATGCCCAT 492
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134 YrAsnLysIleAsnGlnArgIleLeuValValAspProValThrSerGlu 150
493 ACACAAATCAACCAAGAAATTTGGTGTGGATCCAGTCACCTCGAA 542
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151 HisGluLeuThrCysGlnAlaGluGlyTyrProLysAlaGluValIleTr 167
543 CATTGAATGATGATGTCAGGCTGAGGGCTACCCCAAGCGCAATTCATCT 592
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167 pThrSerSerAspHisGlnValLeuSerGlyLysThrThrThrAsnS 184
593 GACAAACAGAGACCAATCAAGTCTGAGTGTAGACCAACCAACCAAAAT 641
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184 eTrpAspGluGluLysLeuPheAsnValThrSerThrLeuArgIleAsn 200
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AC AAS05933:
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DT 26-SEP-2001 (first entry)
XX
DE Mouse immunoregulatory protein B7-H1 cDNA sequence.
XX
XX
KW Mouse; immunoregulatory protein: B7-H1; co-stimulating 1-cell;
KW B-cell antibody-producing response; IgG2a antibody response; APC;
KW immunodeficiency disease; inflammatory disease; autoimmune disease;
KW antigen presenting cell; pathologic cell mediated disease; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
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Date: Mar 18, 2002 7:27 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-FGAPO=6.000 -FGAPEXT=7.000 -YGAPO=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsoms62
-TRANS=humand0.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

5. Information block:

Query: US-09-649-108-1
Query length: 290
Database: Issued_Patents_NA.*
Database sequences: 351203
Database length: 11328999
Search time (sec): 43.780000

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 ? AUTHORS: WHITMAN, JAMES F.
 ?
 ? AUTHORS: NADLER, LEE M.
 ? TITLE: B7, A New Member Of The Ig Superfamily With
 ? TITLE: Unique Expression On Activated And Neoplastic B Cells
 ? JOURNAL: The Journal of Immunology
 ? VOLUME: 143
 ? ISSUE: 8
 ? PAGES: 2714-2722
 ? DATE: 15-OCT-1989
 ? RELEVANT RESIDUES IN SEQ ID NO: 1 : FROM 1 TO 1491
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; Sequence 28, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandagouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPT-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien

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APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raj1
IMMEDIATE SOURCE:
LIBRARY: cDNA in pCDM8 vector
CLONE: B7, Raj1 clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
FEATURE:
NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
FEATURE:
NAME/KEY: Alternate polyadenylation signal
LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: similarity to other pattern
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 28: FROM 1 TO 1491
US-08-280-757B-28

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Quality: 176.50 Length: 279
Ratio: 1.177 Gaps: 12
Percent Similarity: 53.763 Percent Identity: 21.505

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seq_name: /cgn2_6/prodata/2/lna/6A_COMB.seq:US-09-159-135-1

seq_documentation_block:
; Sequence 1, Application US/09159135
; Patent No. 6149905
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Gilmer, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
IMMEDIATE SOURCE:
LIBRARY: cDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
FEATURE:
NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
FEATURE:
NAME/KEY: Alternate polyadenylation signal
LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: similarity to other pattern
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491

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; Sequence 18, Application us/08205697A
; Patent No. 6218510
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor.
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205, 697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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LOCATION: 318..1181
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seq_documentation_block:
: Sequence 18. Application US/08702525
: Patent No. 6294660
: GENERAL INFORMATION:
: APPLICANT: Sharpe, Sharpe
: APPLICANT: Borfello, Francescopolo
: APPLICANT: Freeman, Gordon
: APPLICANT: Nadler, Lee
: TITLE OF INVENTION: NO. 6294660el Forms of T Cell Costimulatory
: TITLE OF INVENTION: Molecules and uses Therefor
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts

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TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 18:


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; Sequence 207, Application US/08458356
; Patent No. 5942235

; GENERAL INFORMATION:

; APPLICANT: Proietti, Enzo
; APPLICANT: Tartaglia, James

; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY

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? NUMBER OF SEQUENCES: 217
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Curtis Morris & Salford
? STREET: 530 Fifth Avenue
? CITY: New York
? STATE: NY
? COUNTRY: USA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/458,356
? FILING DATE: 02-JUN-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/184,009
? FILING DATE: 19-JAN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Frommer, William S.
? REGISTRATION NUMBER: 25,506
? REFERENCE/DOCKET NUMBER: 454310-2530
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 840-3333
? TELEFAX: (212) 840-0712
?
? INFORMATION FOR SEQ ID NO: 207:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 867 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? US-08-458-356-207

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alignment_scores:

Quality: 172.00 Length: 263
Ratio: 1.178 Gaps: 12
Percent Similarity: 55.513 Percent Identity: 22.053

alignment_block:

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Align seg 1/1 to: US-08-458-356-207 from: 1 to: 867

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41 sphenovalglulysglinleuaspheuaialaleuilevaltyrtrg 58
172 .....GAGCTGGCACAACCTCCCATCTACTGCGC 199
58 lunetgluasplysasnillelelnphevalhlsiglygluinspleu 74
200 AAAGAGAGAAATGGTCTGACTATGATGCTGGGACATGAAATA 249
75 lysvalglhissersertyrarglnargalargleuleuylsaspgl 91
250 TGGCCCGAGTACAAGAAC.....CGAGCATCTTTGAT.. 282
91 nleuserleuglyasnalaaleuqlnlethraspyalllysleuglna 108
283 ....ATCACTAATACCTCTCCATTTGATGATCTGGCTCGGCCCATCTG 328
108 spaliaglyvaltyrargyemetile...sertyrglyalalaaspyr 123
329 ACAGGGCCACATACGAGTGTGTCTGAGATGAAAAAGACGCTTTC 378
124 lysarg.....lethrvallysalasnalapr 133

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150 LnhISGluLeuThrCysGlnAlaGlu...GlyTyrProLysAlaGluVal 165
470 TTGAAGGATTAATTTGCTCAACCTCGAGGTTTCCAGAGCCTCACCTC 519
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520 TCCTGGTTGGAAATGGAGAGAA...TTAAATGCCATCAACACACACAGT 566
182 rAsnSerLysArgGluGluLysLeuPheAsnValThrSerThrLeuArg 199
567 TTCCCAAGATCCTGGAACAGCTGATGCTGTATGACACCAACAGTGAT 616
199 lEAsnThrThrThrAsnGluIlePheTyrCys..... 209
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210 .....ThrPheArgArgLeuAspProGluGlnAsnHisThr 221
667 TTAAGAGTAATCAGACCTTCACTGGAATACACCAACAGACAGATTT 716
717 TCCTGATACCTGCTCCATCTCGGCCCAT..... 747
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748 ..ACCTTAATCTCAGTAATGGAATTTTGTGATATGC.....TGC 786
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seq_name: /cgn2_6/plodata/2/lna/6B_COMB.seq:us-08-812-946A-2

seq_documentation_block:
: Sequence 2, Application us/08812946A
: Patent No. 6221637
: GENERAL INFORMATION:
: APPLICANT: Tsuneaki HIDA et al.
: TITLE OF INVENTION: XANTHENE DERIVATIVES, THEIR PRODUCTION AND
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wenderoth, Lind & Ponack
: STREET: 805 Fifteenth Street, N.W., #700
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/812,946A
: FILING DATE: March 4, 1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warren M. Cheek, Jr.
: REGISTRATION NUMBER: 33,367
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:

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: TELEPHONE: 202-371-8850
: TELEX:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 867 bases
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-812-946A-2

alignment_scores:
Quality: 172.00 Length: 263
Ratio: 1.178 Gaps: 12
Percent Similarity: 55.513 Percent Identity: 22.053

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41 sPheProValGluLysGlnLeuAspLeuAlaLeuIleValTyrTrpG 58
172 .....GAGCTGGCACAACTCGCATCTACTGTGCGC 199
58 lMetGluAspLysAsnIleIleGlnPheValHisGlyGluGlnAspLeu 74
200 AAAGAAGTGGCAAAATGTTGCTGCTGATGATGTCGCGGACATGTAATVA 249
75 LysValGlnHisSerSerTyrArgGlnArgAlaArgLeuLeuLysAsp 51
250 TGGCCCGAGTACAGAC.....CGACCATCTTTGAT.. 282
91 nLeuSerLeuGlyAsnAlaAlaLeuGlnIleThrAspValLysLeuGlu 108
283 ...ATCACTAATTAACCTCTCCATTTGTATCTCGGCTCGCGCCATCTG 748
108 sPAlaGlyValTyrArgCysMetIle...SerTyrGlyGlnAlaAspTyr 123
329 ACGAGGCGACATACGAGTGTGTTGTCGAAAGTGAACAAACACCC1TTC 378
124 LysArg.....lIeThrValLysValAsnAlaTrp 133
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133 CTYrAnLysIleAsnGlnArgIleLeuValValAspProValThrSerG 150
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150 LnhISGluLeuThrCysGlnAlaGlu...GlyTyrProLysAlaGluVal 165
470 TTGAAGGATTAATTTGCTCAACCTCGAGGTTTCCAGAGCCTCACCTC 519
166 lIeTrpThrSerSerAspHisGlnValLeuSerGlyLysThrThrThr 182
520 TCCTGGTTGGAAATGGAGAGAA...TTAAATGCCATCAACACACAGT 566
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567 TTCCCAAGATCCTGGAACAGCTGATGCTGTATGACACCAACAGTGAT 616
199 lEAsnThrThrThrAsnGluIlePheTyrCys..... 209
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seq_documentation_block:
; Sequence 207, Application US/08460736
; Patent No. 6265189
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,736
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/184,009
; FILING DATE: 19-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 207:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 867 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-460-736-207

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US-09-649-108-1 x US-08-460-736-207

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25 LysAspLeuTyrValValGluTyrGlySerAsnMetThrIleGluCysLys 41

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41 sPheProValGluLysGlnLeuAspLeuAlaIleValTyrTrpG 58
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58 LmetGluAspLysAsnIleIleGlnPheValHisGlyGluLysAspLeu 74
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75 LysValGlnHisSerSerTyrArgGlnArgAlaArgLeuLysAspL 51
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91 nLeuSerLeuGlyAsnAlaIleLeuGlnIleThrAspValLysLeuGln 108
283 ....ATCACTAATTAACCTCTCATTTGTGATCCTGGCTCGCCCATCTG 328
108 sPAlaGlyValTyrArgCysMetIle..SerTyrGlyGlyAlaAsp 123
329 ACGAGGACATACGATGCTGTGTTGTCGAGATGAAAAAGACCTTTC 378
124 LysArg.....IleThrValLysValAsnAlaArg 133
379 AAGCGGACACCTGGCTGAGTGAAGTATGATGCAAGTCAGATGATGCC 428
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429 TACACCTACTATATCTGACTTGAATTT.....CCACTTCATATA 469
150 LHisGluLeuThrCysGlnAlaGlu..GlyTyrProLysAlaGluVal 165
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